

10/510903

10/510903

SEQ ID NO:1

Size: 410

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```

FIG. 1 (1/2)

10/510903_

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3301 aagacaaccc gttggagccc ctgtgttcca gaggacctga tgccaagggg taatgggccc
3361 agcagtgcct ctggagccca ggccccaaca cagcccatg gcctctgcca gatggctttg
3421 aaaaagggtga tccaagcagg cccctttatc tgtacatagt gactgagtgg ggggtgctgg
3481 caagtgtggc agctgcctct gggctgagca cagcttgacc cctctagccc ctgtaaatac
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SEQ ID NO:2

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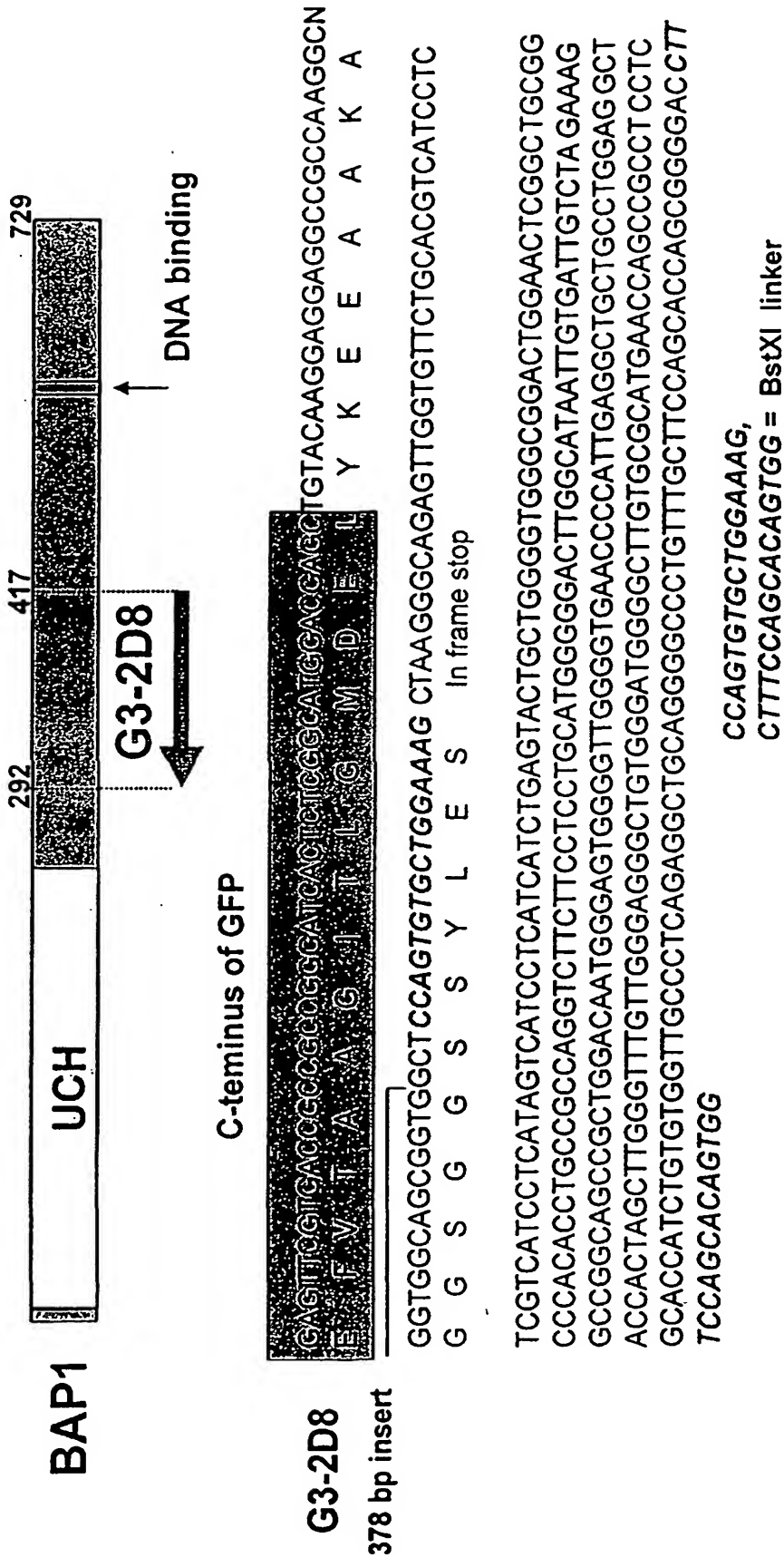
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IRFNLMAVVPDRRIKYEARLHVLKVNROTVEALQQLIRVTQPELIQTHKSQESQLPEESKSASNKSPVLEANR
APAASEGNHTDGAEAAAGSCAQAPSHSPNPKPLVVKPPGSSLNGVHPNPTPIVQRLPAFLDNHNYAKSPMQEEE
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HISKVLFGEDDSLRLVDCIRYNRAVRDLGPVISTGLLHLAEDGVLSPALTEGGKGSSPSIRPIQGSQGSSSPVE
KEVVEATDSREKTGMVRPGEPLSGEKYSPKELLALLKCVEAEIANYEACLKEEVEKRKKFKIDDQRRTHNYDEFI
CTFISMLAQEGMLANLVEQNISVRRRQGVSIGRLHKQRPDRRKRSRPHYKAKRQ

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G3-2D8 / BRCA1-Associated Protein-1 (BAP1)

The G3-2D8 sequence is identical to BRCA1-Associated Protein-1 (BAP1), 729aa
Orientation: Antisense

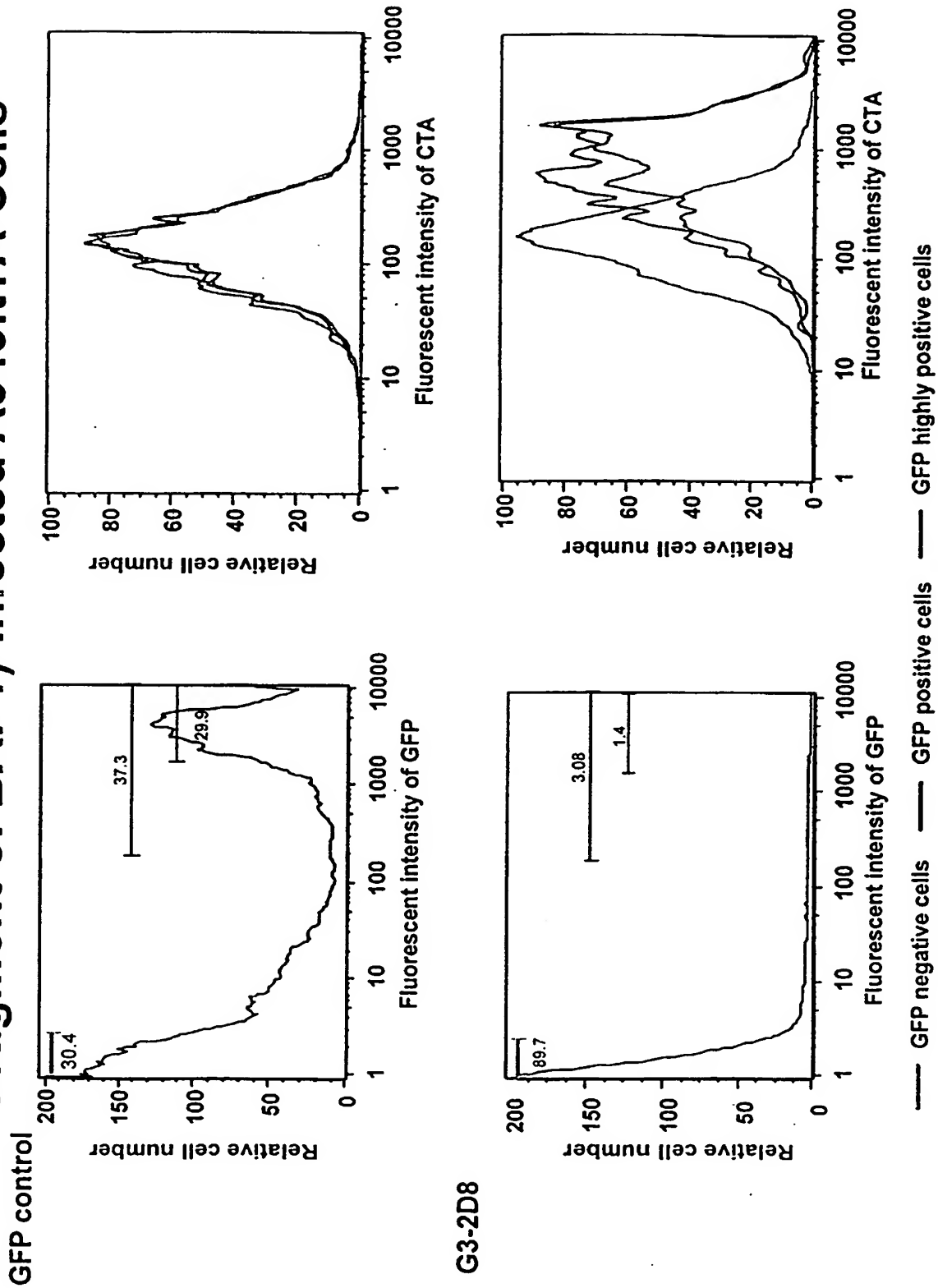


UCH(4-216): Ubiquitin carboxyl-terminal hydrolase, family 1,
DNA binding (625-640): 7kD DNA-binding domain

FIG. 2

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Cell Tracker Analysis of G3-2D8 (The Antisense Fragment of BAP1)-Infected A549.tTA Cells



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SEQ ID NO:3

Size: 437

DNA--NP95

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121  ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAAGATC
181  CAGGAGCTGT TCCACGTGGA GCCAGGCCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG
241  GAGGACGGCC ATACCCTCTT CGACTACGAG GTCCGCCTGA ATGACACCAT CCAGCTCCTG
301  GTCCGCCAGA GCCTCGTGCT CCCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC
361  ACCGACTCCG GCTGCTGCCT GGGCCAGAGT GAGTCAGACA AGTCCTCCAC CCACGGCGAG
421  GCGGCCGCCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG
481  GGGCTGTACA AGGTCAATGA GTACGTCGAT GCTCGGGACA CGAACATGGG GCGCTGGTTT
541  GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCTCCC GGGACGAGCC CTGCAGCTCC
601  ACGTCCAGGC CGGCGCTGGA GGAGGACGTC ATTTACCACG TGAAATACGA CGACTACCCG
661  GAGAACGGCG TGGTCCAGAT GAACTCCAGG GACGTCGAG CGCGCGCCCG CACCATCATC
721  AAGTGGCAGG ACCTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC
781  AAGGAGCGGG GCTTCTGGTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGCG
841  CGGGAACCTT ACGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC
901  TTCGTGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCCAT GGTTGACAAC
961  CCCATGAGAC GGAAGAGCGG GCCGTCTGTC AAGCACTGCA AGGACGACGT GAACAGACTC
1021  TGCCGGGTCT GCGCCTGCCA CCTGTGCGGG GGCCGGCAGG ACCCCGACAA GCAGCTCATG
1081  TGCATGAGT GCGACATGGC CTTCACATC TACTGCCTGG ACCCGCCCCT CAGCAGTGTT
1141  CCCAGCGAGG ACGAGTGTA CTGCCCTGAG TGCCGGAATG ATGCCAGCGA GGTGGTACTG
1201  GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCCTCGGC CACATCGTCC
1261  TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC
1321  GTCCCGTCCA ACCACTACGG ACCCATCCCC GGGATCCCCG TGGGCACCAT GTGGCGGTTT
1381  CGAGTCCAGG TCAGCGAGTC GGGTGTCCAT CGGCCCCACG TGGCTGGCAT ACACGGCCGG
1441  AGCAACGACG GAGCGTACTC CCTAGTCCCT GCGGGGGGCT ATGAGGATGA CGTGGACCAT
1501  GGGAAATTTT TCACATACAC GGGTAGTGGT GGTGAGATC TTTCCGCAA CAAGAGGACC
1561  GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC
1621  TTTGCTCCCA TCAATGACCA AGAAGGGGCG GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG
1681  GTCAGGGTGG TGCGCAATGT CAAGGGTGGC AGAATAGCA AGTACGCCCC CGCTGAGGGC
1741  AACCCTACG ATGGCATCTA CAAGGTTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG
1801  TTTCTCGTGT GCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG
1861  GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG
1921  GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGGAGGA GGAGGAGCAG
1981  CAGGAGGGGG GCTTCGCGTC CCCCAGGACG GGCAAGGGCA AGTGGAAGCG GAAGTCGGCA
2041  GGAGGTGGCC CGAGCAGGGC CGGGTCCCCG CGCCGGACAT CCAAGAAAAC CAAGGTGGAG
2101  CCCTACAGTC TCACGGCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG
2161  CTGTGGAATG AGGTCTGGC GTCACTCAAG GACCGGCCGG CGAGCGGCAG CCCGTTCCAG
2221  TTGTTCTGTA GTAAAGTGGA GGAGACGTTT CAGTGTATCT GCTGTGAGG GCTGGTGTTC
2281  CGGCCCATCA CGACCGTGTG CCAGCACAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT
2341  CGGGCACAGG TGTTCACTG CCCTGCCTGC CGCTACGACC TGGGCCGAG CTATGCCATG
2401  CAGGTGAACC AGCCTCTGCA GACCGTCTCT AACCAGCTCT TCCCCGCTA CGGCAATGGC
2461  CGGTGATCTC CAAGCACTTC TCGACAGGCG TTTTGCTGAA AACGTGTCGG AGGGCTCGTT
2521  CATCGGCACT GATTTTGTTC TTAGTGGGCT TAACTTAAAC AGGTAGTGTT TCCTCCGTTT
2581  CCTAAAAGG TTTGTCTTCC TTTTCTTTTA TTTTATTTT TCAAATCTAT ACATTTTCAG
2641  GAATTTATGT ATTCTGGCTA AAAGTTGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAAA
2701  CATAAAAGCC TGCAATTTCT CGACAAAACA ACACAAGATT TTTTAAAGAT GGAATCAGAA
2761  ACTACGTGGT GTGGAGGCTG TTGATGTTTC TGGTGTCAAG TTCTCAGAAG TTCTGCCAC
2821  CAACTCTTTA AGAAGGCGAC AGGATCAGTC CTTCTCTAGG GTTCTGGCCC CCAAGGTCAG
2881  AGCAAGCATC TTCCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCCGTGG
2941  TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTGTAAGTT GTTGCAAGGA
3001  AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTTGCCTC AAAGCCATCC CCCACCAGAC
3061  TGCTTAGCGT CTGAGATCCG CGTGAAAAGT CCTCTGCCCA CGAGAGCAGG GAGTTGGGGC
3121  CACGCAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGAATGACGC
```

FIG. 4 (1/2)

10/510903

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3241 GATTCGTTCC TTCTTCTAA AGACGACAGT CTTTGTGTGTT AGCACTGAAT TATTGAAAAT
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3361 GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCAATTTT TTAACTCAG CAAGTGAGAA
3421 CTTACAAGAG GGTTTTTTTT TAATTTTTTT TTCTCTTAAT GAACACATTT TCTAAATGAA
3481 TTTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACGTTAGGGT TTGGTTGTTT
3541 TTGTTTTTGT ATTTTTTTTC TTTTGAAAGG GTTTGTTAAT TTTTCTAATT TTACCAAAGT
3601 TTGCAGCCTA TACCTCAATA AAACAGGGAT ATTTTAAATC ACATACCTGC AGACAAACTG
3661 GAGCAATGTT ATTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT
3721 AGGGAAGAAT GAGACAATTT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCCAGATT
3781 TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAA AAAAAAA

SEQ ID NO:4

Size: 135

PRT--NP95

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FIG. 4 (2/2)

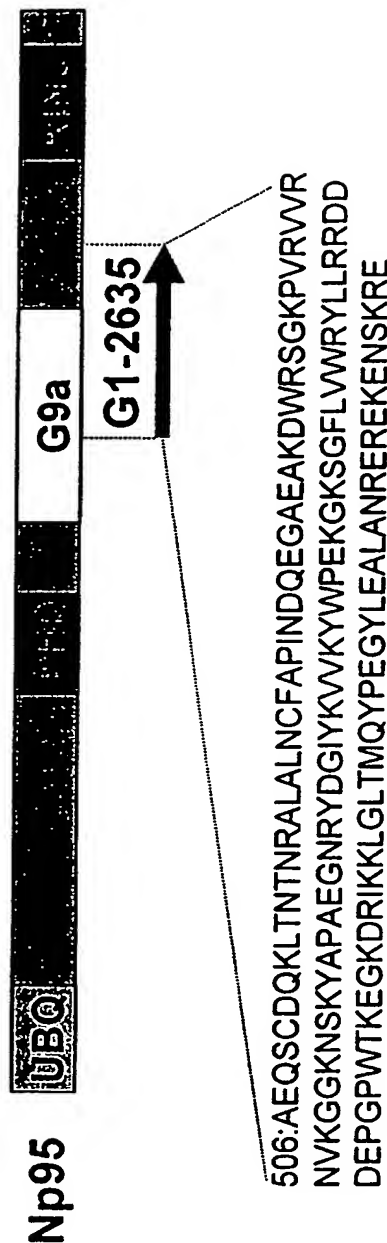
10/510903

G1-2635 / Np95

The G1-2635 sequence is identical to a nuclear zinc finger protein, Np95, 793aa

Orientation of cDNA: Sense

Pfam HMM search was done at the Washington University web site



UBQ(14-89): Ubiquitin like domain,
PHD(330-379): PHD-Zn finger, It could be important for the assembly or activity of multicomponent complexes
G9a(427-599): It is found in a nuclear protein associated with cell proliferation
RING(737-775): Zinc finger, C3HC4 type (RING finger), E3 ubiquitin-protein ligase activity is intrinsic to the RING domain of c-Cbl and is likely to be a general function of this domain; Various RING fingers exhibit binding to E2 ubiquitin-conjugating enzymes

FIG. 5

Cell Tracker Analysis of G1-2635 (The Fragment of Np95)-Infected A549.tTA Cells

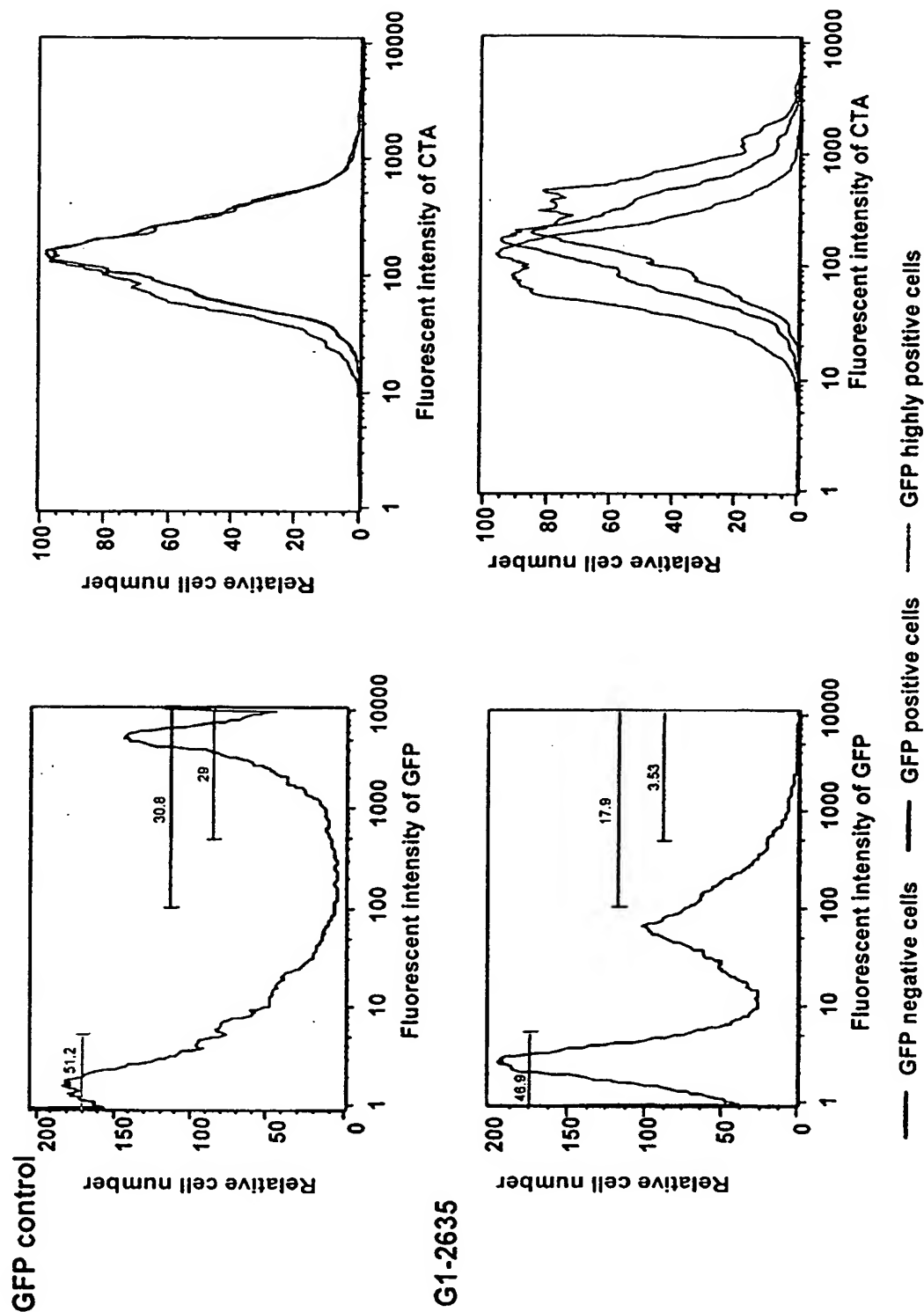





FIG. 6

FIG. 7 (1/5)

10/510903

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM 8

Search for

Limits Preview/Index History Clipboard Details

Display

1: NM_000135. Homo sapiens Related Sequences, OMIM, Protein, PubMed, Taxonomy, UniSTS, LinkOut

Fanc...[gi:4503654]

LOCUS NM_000135 5503 bp mRNA linear PRI 05-JUL-2001
 DEFINITION Homo sapiens Fanconi anemia, complementation group A (FANCA), mRNA.
 ACCESSION NM_000135
 VERSION NM_000135.1 GI:4503654

FANCA

KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5503)
 AUTHORS Pronk JC, Gibson RA, Savoia A, Wijker M, Morgan NV, Melchionda S, Ford D, Temtamy S, Ortega JJ, Jansen S and et al.
 TITLE Localisation of the Fanconi anaemia complementation group A gene to chromosome 16q24.3
 JOURNAL Nat. Genet. 11 (3), 338-340 (1995)
 MEDLINE 96042586
 PUBMED 7581462

REFERENCE 2 (bases 1 to 5503)
 AUTHORS Lo Ten Foe, J.R., Rooimans, M.A., Bosnoyan-Collins, L., Alon, N., Wijker, M., Parker, L., Lightfoot, J., Carreau, M., Callen, D.F., Savoia, A., Cheng, N.C., Van Berkel, C.G.M., Strunk, M.H.P., Gille, J.J.P., Pals, G., Kruyt, F.A.E., Pronk, J.C., Arwert, F., Buchwald, M. and Joenje, H.
 TITLE Expression cloning of a cDNA for the major Fanconi anaemia gene, FAA
 JOURNAL Nat. Genet. 14 (3), 320-323 (1996)
 MEDLINE 97051928

REFERENCE 3 (bases 1 to 5503)
 AUTHORS Ianzano L, D'Apolito M, Centra M, Savino M, Levrano O, Auerbach AD, Cleton-Jansen AM, Doggett NA, Pronk JC, Tipping AJ, Gibson RA, Mathew CG, Whitmore SA, Apostolou S, Callen DF, Zelante L and Savoia A.
 TITLE The genomic organization of the Fanconi anemia group A (FAA) gene
 JOURNAL Genomics 41 (3), 309-314 (1997)
 MEDLINE 97312685
 PUBMED 9169126

REFERENCE 4 (bases 1 to 5503)
 AUTHORS Joenje H, Oostra AB, Wijker M, di Summa FM, van Berkel CG, Rooimans MA, Ebell W, van Weel M, Pronk JC, Buchwald M and Arwert F.
 TITLE Evidence for at least eight Fanconi anemia genes
 JOURNAL Am. J. Hum. Genet. 61 (4), 940-944 (1997)
 MEDLINE 98018453
 PUBMED 9382107

REFERENCE 5 (bases 1 to 5503)
 AUTHORS Kupfer GM, Naf D, Suliman A, Pulsipher M and D'Andrea AD.
 TITLE The Fanconi anaemia proteins, FAA and FAC, interact to form a

nuclear complex
JOURNAL Nat. Genet. 17 (4), 487-490 (1997)
MEDLINE 98061104
PUBMED 9398857
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from X99226.1.
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VLCGSSFQAEQPI TARCEQFFHLVNSEMRNFCSHGGALTQDITAHFFRGLLNACLRSR
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FIG. 7 (3/5)

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BASE COUNT 1208 a 1527 c 1492 g 1276 t
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```

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FIG. 7 (4/5)

```

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1921 gaagccagaa gatgcagccc tgggagttag ggcagaaccc aactctgctg aggagccct
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5341 gcctcgttta ttaagatctt taaactgctt tatacactgt cacgtggctt catcagctgt

```


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FIG. 7 (5/5)

5401 gtgcatttca ggatggtttt taaagaaacc tcagaaagct atttccttaa aaaaaaaaaa
5461 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa

//

Revised: October 24, 2001.

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FIG. 8 (1/4)

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Nucleotide

PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

8

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Details

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default

Save

Text

Add to clipboard

1: NM_030588. Homo sapiens
DEAD...[gi:13514821]

Related Sequences, OMIM, Protein, PubMed, Taxonomy,
UniSTS, LinkOut

LOCUS NM_030588 1378 bp mRNA linear PRI 02-APR-2001

DEFINITION Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 2, mRNA.

ACCESSION NM_030588

VERSION NM_030588.1 GI:13514821

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1378)

AUTHORS Lee, C.G. and Hurwitz, J.

TITLE A new RNA helicase isolated from HeLa cells that catalytically translocates in the 3' to 5' direction

JOURNAL J. Biol. Chem. 267 (7), 4398-4407 (1992)

MEDLINE 92165790

PUBMED 1537828

REFERENCE 2 (bases 1 to 1378)

AUTHORS Lee, C.G., Zamore, P.D., Green, M.R. and Hurwitz, J.

TITLE RNA annealing activity is intrinsically associated with U2AF

JOURNAL J. Biol. Chem. 268 (18), 13472-13478 (1993)

MEDLINE 93293869

PUBMED 7685763

REFERENCE 3 (bases 1 to 1378)

AUTHORS Lee, C.G. and Hurwitz, J.

TITLE Human RNA helicase A is homologous to the maleless protein of Drosophila

JOURNAL J. Biol. Chem. 268 (22), 16822-16830 (1993)

MEDLINE 93346440

PUBMED 8344961

REFERENCE 4 (bases 1 to 1378)

AUTHORS Abdelhaleem, M.M., Hameed, S., Klassen, D. and Greenberg, A.H.

TITLE Leukophysin: an RNA helicase A-related molecule identified in cytotoxic T cell granules and vesicles

JOURNAL J. Immunol. 156 (6), 2026-2035 (1996)

MEDLINE 96310937

PUBMED 8690889

REFERENCE 5 (bases 1 to 1378)

AUTHORS Zhang, S. and Grosse, F.

TITLE Domain structure of human nuclear DNA helicase II (RNA helicase A)

JOURNAL J. Biol. Chem. 272 (17), 11487-11494 (1997)

MEDLINE 97269062

PUBMED 9111062

REFERENCE 6 (bases 1 to 1378)

AUTHORS Nakajima, T., Uchida, C., Anderson, S.F., Lee, C.G., Hurwitz, J.,

DDX9

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FIG. 8 (2/4)

Parvin, J.D. and Montminy, M.
TITLE RNA helicase A mediates association of CBP with RNA polymerase II
JOURNAL Cell 90 (6), 1107-1112 (1997)
MEDLINE 97462911
PUBMED 9323138
REFERENCE 7 (bases 1 to 1378)
AUTHORS Lee, C.G., da Costa Soares, V., Newberger, C., Manova, K., Lacy, E. and Hurwitz, J.

TITLE RNA helicase A is essential for normal gastrulation
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13709-13713 (1998)
MEDLINE 99030634
PUBMED 9811865
REFERENCE 8 (bases 1 to 1378)
AUTHORS Lee, C.G., Eki, T., Okumura, K., Nogami, M., Soares, Vd., Murakami, Y., Hanaoka, F. and Hurwitz, J.

TITLE The human RNA helicase A (DDX9) gene maps to the prostate cancer susceptibility locus at chromosome band 1q25 and its pseudogene (DDX9P) to 13q22, respectively
JOURNAL Somat. Cell Mol. Genet. 25 (1), 33-39 (1999)
MEDLINE 20381755
PUBMED 10925702

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from U03643.1.
 Summary: DEAD box proteins, characterized by the conserved motif Asp-Glu-Ala-Asp (DEAD), are putative RNA helicases. They are implicated in a number of cellular processes involving alteration of RNA secondary structure such as translation initiation, nuclear and mitochondrial splicing, and ribosome and spliceosome assembly. Based on their distribution patterns, some members of this family are believed to be involved in embryogenesis, spermatogenesis, and cellular growth and division. This gene includes 2 alternatively spliced transcripts, encoding 2 different isoforms. The larger isoform is a DEAD box protein with RNA helicase activity. It may participate in melting of DNA:RNA hybrids, such as those that occur during transcription, and may play a role in X-linked gene expression. It contains 2 copies of a double-stranded RNA-binding domain, a DEXH core domain and an RGG box. The RNA-binding domains and RGG box influence and regulate RNA helicase activity. The smaller isoform is a lymphocyte granule protein. It lacks RNA-binding domains and DEXH core domain, but contains an RGG box, which may render this isoform RNA binding function.
 Transcript Variant: This variant (2) is missing a 104 nt internal fragment, in addition to 2722 nt in the 5' UTR, as compared to variant 1. It encodes the smaller isoform, which is associated with lymphocyte granules.
 COMPLETENESS: complete on the 3' end.

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FIG. 8 (3/4)

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 /db_xref="MIM:603115"
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 isoform 2"
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 ORIGIN

10/510903

FIG. 8 (4/4)

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421 aaaggcatga cttagtcac cccctgcag ttgcttctct ttgcctccaa gaaagtccaa
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1321 ataacttggg attttctctg ctttcgttta atacaataga aaataaagta ttacaccg

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Revised: October 24, 2001.

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FIG. 9 (1/6)



Nucleotide

Search Nucleotide for Go Clear

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Display default Save Text Add to clipboard

1: NM_000875. Homo sapiens
insu...[gi:11068002]

Related Sequences, OMIM, Protein, PubMed, Taxonomy,
UniSTS, LinkOut

LOCUS NM_000875 4989 bp mRNA linear PRI 01-NOV-2000
 DEFINITION Homo sapiens insulin-like growth factor 1 receptor (IGF1R), mRNA.
 ACCESSION NM_000875
 VERSION NM_000875.2 GI:11068002
 KEYWORDS IGF1-R
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4989)
 AUTHORS Flier JS, Usher P and Moses AC.
 TITLE Monoclonal antibody to the type I insulin-like growth factor
 (IGF-I) receptor blocks IGF-I receptor-mediated DNA synthesis:
 clarification of the mitogenic mechanisms of IGF-I and insulin in
 human skin fibroblasts
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (3), 664-668 (1986)
 MEDLINE 86121000
 PUBMED 3003744

REFERENCE 2 (bases 1 to 4989)
 AUTHORS Francke U, Yang-Feng TL, Brissenden JE and Ullrich A.
 TITLE Chromosomal mapping of genes involved in growth control
 JOURNAL Cold Spring Harb. Symp. Quant. Biol. 51 Pt 2, 855-866 (1986)
 MEDLINE 87217109
 PUBMED 3107886

REFERENCE 3 (bases 1 to 4989)
 AUTHORS Ullrich, A., Gray, A., Tam, A.W., Yang-Feng, T., Tsubokawa, M.,
 Collins, C., Henzel, W., Bon, T.L., Kathuria, S., Chen, E., Jakobs, S.,
 Francke, U., Ramachandran, J. and Fujita-Yamaguchi, Y.
 TITLE Insulin-like growth factor I receptor primary structure: comparison
 with insulin receptor suggests structural determinants that define
 functional specificity
 JOURNAL EMBO J. 5 (10), 2503-2512 (1986)
 MEDLINE 87053815

REFERENCE 4 (bases 1 to 4989)
 AUTHORS Cooke DW, Bankert LA, Roberts CT Jr, LeRoith D and Casella SJ.
 TITLE Analysis of the human type I insulin-like growth factor receptor
 promoter region
 JOURNAL Biochem. Biophys. Res. Commun. 177 (3), 1113-1120 (1991)
 MEDLINE 91282751
 PUBMED 1711844

REFERENCE 5 (bases 1 to 4989)
 AUTHORS Abbott AM, Bueno R, Pedrini MT, Murray JM and Smith RJ.
 TITLE Insulin-like growth factor I receptor gene structure
 JOURNAL J. Biol. Chem. 267 (15), 10759-10763 (1992)
 MEDLINE 92268129
 PUBMED 1316909

FIG. 9 (2/6)

10/510903

REFERENCE 6 (bases 1 to 4989)
 AUTHORS Werner H, Karnieli E, Rauscher FJ and LeRoith D.
 TITLE Wild-type and mutant p53 differentially regulate transcription of the insulin-like growth factor I receptor gene
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (16), 8318-8323 (1996)
 MEDLINE 96323219
 PUBMED 8710868

REFERENCE 7 (bases 1 to 4989)
 AUTHORS Grant ES, Ross MB, Ballard S, Naylor A and Habib FK.
 TITLE The insulin-like growth factor type I receptor stimulates growth and suppresses apoptosis in prostatic stromal cells
 JOURNAL J. Clin. Endocrinol. Metab. 83 (9), 3252-3257 (1998)
 MEDLINE 98417960
 PUBMED 9745438

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from X04434.1, M69229.1.
 On Nov 1, 2000 this sequence version replaced gi:4557664.
 Summary: This receptor binds insulin-like growth factor with a high affinity. It has tyrosine kinase activity. The insulin-like growth factor I receptor plays a critical role in transformation events. Cleavage of the precursor generates alpha and beta subunits. It is highly overexpressed in most malignant tissues where it functions as an anti-apoptotic agent by enhancing cell survival.

FEATURES
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FIG. 9 (3/6)

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misc_feature 434..442
 /note="pot.N-linked glycostlation site (AA 105 - 107)"
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 /note="FU; Region: Furin-like repeats"
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 /note="pot.N-linked glycosylation site (AA 592 - 594)"
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 /note="beta-subunit (AA 711 - 1337)"
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 /note="pot.N-linked glycosylation site (AA 717 - 719)"
misc_feature 2297..2305
 /note="pot.N-linked glycosylation site (AA 726 - 728)"
misc_feature 2321..2329

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FIG. 9 (4/6)

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 2729..2737
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 2768..2776
misc feature /note="pot.N-linked glycosylation site (AA 883 - 885)"
 2836..2910
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 2918..2926
misc feature /note="pot.N-linked glycosylation site (AA 933 - 935)"
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 3047..3049
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 3052..3807
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FIG. 9 (5/6)

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1501 gcctcctgtg aaagtgacgt cctgcatttc acctccacca ccacgtcgaa gaatcgcatc
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```

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FIG. 9 (6/6)

4981 tgaaccggc

//

Revised: October 24, 2001.

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NCBI | NLM | NIH

10/510903

FIG. 10 (1/4)



Nucleotide

PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Search for Display Limits Preview/Index History Clipboard Detail1: NM_003349. Homo sapiens
ubiq...[gi:15718757]Related Sequences, OMIM, Protein, PubMed, Taxonomy,
UniSTS, LinkOut

LOCUS NM_003349 2394 bp mRNA linear PRI 21-SEP-2001

DEFINITION Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1),
transcript variant 2, mRNA.

ACCESSION NM_003349

VERSION NM_003349.3 GI:15718757

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2394)

AUTHORS Rothofsky, M.L. and Lin, S.L.

TITLE CROC-1 encodes a protein which mediates transcriptional activation
of the human FOS promoter

JOURNAL Gene 195 (2), 141-149 (1997)

MEDLINE 97449289

PUBMED 9305758

REFERENCE 2 (bases 1 to 2394)

AUTHORS Sancho, E., Vila, M.R., Sanchez-Pulido, L., Lozano, J.J., Paciucci,
R., Nadal, M., Fox, M., Harvey, C., Bercovich, B., Loukili, N.,
Ciechanover, A., Lin, S.L., Sanz, F., Estivill, X., Valencia, A.
and Thomson, T.M.

TITLE Role of UEV-1, an inactive variant of the E2 ubiquitin-conjugating
enzymes, in in vitro differentiation and cell cycle behavior of
HT-29-M6 intestinal mucosecretory cells

JOURNAL Mol. Cell. Biol. 18 (1), 576-589 (1998)

MEDLINE 98078713

PUBMED 9418904

REFERENCE 3 (bases 1 to 2394)

AUTHORS Ma, L., Broomfield, S., Lavery, C., Lin, S.L., Xiao, W. and Bacchetti, S.

TITLE Up-regulation of CIR1/CROC1 expression upon cell immortalization
and in tumor-derived human cell lines

JOURNAL Oncogene 17 (10), 1321-1326 (1998)

MEDLINE 98442973

PUBMED 9771976

REFERENCE 4 (bases 1 to 2394)

AUTHORS Hofmann, R.M. and Pickart, C.M.

TITLE Noncanonical MMS2-encoded ubiquitin-conjugating enzyme functions in
assembly of novel polyubiquitin chains for DNA repair

JOURNAL Cell 96 (5), 645-653 (1999)

MEDLINE 99189750

PUBMED 10089880

REFERENCE 5 (bases 1 to 2394)

AUTHORS Deng, L., Wang, C., Spencer, E., Yang, L., Braun, A., You, J.,
Slaughter, C., Pickart, C. and Chen, Z.J.

TITLE Activation of the IkappaB kinase complex by TRAF6 requires a

10/510903

FIG. 10 (2/4)

dimeric ubiquitin-conjugating enzyme complex and a unique polyubiquitin chain

JOURNAL Cell 103 (2), 351-361 (2000)

MEDLINE 20509589

PUBMED 11057907

REFERENCE 6 (bases 1 to 2394)

AUTHORS Thomson,T.M., Lozano,J.J., Loukili,N., Carrio,R., Serras,F., Cormand,B., Valeri,M., Diaz,V.M., Abril,J., Burset,M., Merino,J., Macaya,A., Corominas,M. and Guigo,R.

TITLE Fusion of the human gene for the polyubiquitination coeffectector UEV1 with Kua, a newly identified gene

JOURNAL Genome Res. 10 (11), 1743-1756 (2000)

MEDLINE 20530912

PUBMED 11076860

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from U39361.1, AL110132.1. On Sep 21, 2001 this sequence version replaced gi:12025659. Summary: Ubiquitin-conjugating enzyme E2 variant proteins constitute a distinct subfamily within the E2 protein family. They have sequence similarity to other ubiquitin-conjugating enzymes but lack the conserved cysteine residue that is critical for the catalytic activity of E2s. The protein encoded by this gene is located in the nucleus and can cause transcriptional activation of the human FOS proto-oncogene. It is thought to be involved in the control of differentiation by altering cell cycle behaviour. Multiple alternatively spliced transcripts encoding different isoforms have been described for this gene. Transcript Variant: This variant (2) encodes the longest isoform (b) of this protein. COMPLETENESS: complete on the 3' end.

FEATURES

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FIG. 10 (3/4)

10/510903

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BASE COUNT 658 a 605 c 481 g 650 t
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421 acacttacaa gatggacagg gatgataatt gggcctccaa gaacaattta tgaaaaccga
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721 tgttacagca attaatacaa aagaaaaacc acaggccctt ccccttcccc ccaattcgat
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FIG. 10 (4/4)

841 gtaccggaaa ggaagctccc attcaaagga aatttatctt aagatactgt aaatgataact
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961 accactgtcc acgtagttga acttctggga tcaagaaagt ctattttaa atgattcccat
1021 cataactggg ggggcacatc taactcaact gtgaaaagac acatcacaca atcaccttgc
1081 tgctgattac acggcctggg gtctctgcct tctcccttta cctcccgc tcccaccctc
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1201 cgcagcctgt gggactactg ctaggtgtgt ggggtgtttc gcctgcacc ctggttcctt
1261 taagtcttaa gtgatgcccc ttccaaacca tcatcctgtc cccacgtcc tccactccc
1321 cccttgcccg aagcatagat tgtaaccctt cactccct ctgagattgg cttcgggtgag
1381 gaattcaggg ctttcccat atcttctct cccaccct tatcgagggg tgctgctttt
1441 tctccctcct cctcaagttc ctttttgac cgtcaccacc caacacttc catgacactt
1501 ccttgctttg gccagaagcc atcaggtgaa gttggaaaga gcctctgacc tcccttggtt
1561 agttttggaa ccatactcac tcaactctca ccagcctggg aaatgaatat tgggtcctca
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1861 tttgggtcatc cttgcaatcc attggggtct agtttgaat ctgcttccca agatcctcag
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2161 tagtatttgt gtaaaaccac cttttgaagc agcaactatc aagtctgaaa agcaattgat
2221 gtttccatta atctttttct ggggggaaaa ccttagttct aaggatttaa catcctgtaa
2281 gtgaagttta acataacagt attccataag cagccttttt attgtcagac cattgcctga
2341 ttttaatatata ataaaaaaaa agtgtgcgtt aataaaaaaaaa aaaaaaaaaa aaaa

//

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10/510903



FIG. 11 (1/3)



Nucleotide

Search for

Display

1: NM_000689. Homo sapiens
alde...[gi:4502030]

Related Sequences, OMIM, Protein, PubMed, Taxonomy,
LinkOut

LOCUS NM_000689 1506 bp mRNA linear PRI 31-OCT-2000
 DEFINITION Homo sapiens aldehyde dehydrogenase 1, soluble (ALDH1), mRNA.
 ACCESSION NM_000689
 VERSION NM_000689.1 GI:4502030
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

ALDEHYDE DEHYDROGENASE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1506)
 AUTHORS Hsu LC, Tani K, Fujiyoshi T, Kurachi K and Yoshida A.
 TITLE Cloning of cDNAs for human aldehyde dehydrogenases 1 and 2
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (11), 3771-3775 (1985)
 MEDLINE 85216574
 PUBMED 2987944

REFERENCE 2 (bases 1 to 1506)
 AUTHORS Raghunathan L, Hsu LC, Klisak I, Sparkes RS, Yoshida A and Mohandas T.
 TITLE Regional localization of the human genes for aldehyde dehydrogenase-1 and aldehyde dehydrogenase-2
 JOURNAL Genomics 2 (3), 267-269 (1988)
 MEDLINE 88284707
 PUBMED 3397064

REFERENCE 3 (bases 1 to 1506)
 AUTHORS Hsu LC, Chang WC and Yoshida A.
 TITLE Genomic structure of the human cytosolic aldehyde dehydrogenase gene
 JOURNAL Genomics 5 (4), 857-865 (1989)
 MEDLINE 90077427
 PUBMED 2591967

REFERENCE 4 (bases 1 to 1506)
 AUTHORS Pereira F, Rosenmann E, Nylen E, Kaufman M, Pinsky L and Wrogemann K.
 TITLE The 56 kDa androgen binding protein is an aldehyde dehydrogenase
 JOURNAL Biochem. Biophys. Res. Commun. 175 (3), 831-838 (1991)
 MEDLINE 91222190
 PUBMED 1709013

REFERENCE 5 (bases 1 to 1506)
 AUTHORS Zheng, C.F., Wang, T.T. and Weiner, H.
 TITLE Cloning and expression of the full-length cDNAs encoding human liver class 1 and class 2 aldehyde dehydrogenase
 JOURNAL Alcohol. Clin. Exp. Res. 17 (4), 828-831 (1993)
 MEDLINE 94027752

REFERENCE 6 (bases 1 to 1506)
 AUTHORS Kathmann, E.C. and Lipsky, J.J.
 TITLE Cloning of a cDNA encoding a constitutively expressed rat liver

FIG. 11 (2/3)

10/510903

cytosolic aldehyde dehydrogenase
JOURNAL Biochem. Biophys. Res. Commun. 236 (2), 527-531 (1997)
MEDLINE 97382470
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from AF003341.1.
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 PLTPGVTQGPQIDKEQYDKILDLESKGKKEGAKLECGGGPWGNGKGYFVQPTVFSNVTD
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 181 gacaaggcag tgaaggccgc aagacaggct tttcagattg gatctccgtg gcgtactatg
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 361 agtgatttag caggctgcat caaacattg cgctactgtg cagggtgggc tgacaagatc
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10/510903

FIG. 11 (3/3)

```
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661 attgttcctg gttatgggcc tacagcaggg gcagccattt cttctcacat ggatatagac
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841 gatgccgact tggacaatgc tgttgaattt gcacaccatg gggatttcta ccaccagggc
901 cagtgttgta tagccgcac caggattttt gtggaagaat caatttatga tgagtttgtt
961 cgaaggagtg ttgagcgggc taagaagtat atccttgga atcctctgac cccaggagtc
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1501 tcataa
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FIG. 12 (1/2)

Nucleotide

PubMed Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

B

Search Nucleotide for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display default

Save Text

Add to Clipboard

1: XM_037768. Homo sapiens simi...[gi:14750404]

Related Sequences, Protein, Taxonomy, LinkOut

LOCUS XM_037768 2282 bp mRNA linear PRI 07-FEB-2002
 DEFINITION Homo sapiens similar to pyruvate kinase, muscle (H. sapiens)
 (LOC145710), mRNA.

ACCESSION XM_037768
 VERSION XM_037768.1 GI:14750404

PYRUVATE KINASE

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2282)

AUTHORS NCBI Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology

Information, NIH, Bethesda, MD 20894, USA

COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was
 predicted from NCBI contig NT_010235 by automated computational
 analysis using gene prediction method: BLAST. -Also see:-
 Documentation of NCBI's Annotation Process- Evidence Viewer :
 alignments supporting this model.

FEATURES

Location/Qualifiers

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/db_xref="InterimID:145710"

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YKNICKVVEVGSKIYVDDGLISLQVKQKGADFLVTEVENGGSLSKKGVNLPGAAVDL

PAVSEKDIQDLKFGVEQDVMVFASFIRKASDVHEVRKVLGEKGKNIKIISKIENHEG

VRRFDEILEASDGIMVARGDLGIEIPAEEKVFLAQKMMIGRCNRAGKPVICATQMLESM

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misc feature

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FIG. 12 (2/2)

10/510903

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2281 gc

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10/510903



FIG. 13 (1/3)



Nucleotide

☐ PubMed ☒ Nucleotide ☐ Protein ☐ Genome ☐ Structure ☐ PopSet ☐ Taxonomy ☐ OMIM ☐ B

Search for

1: XM_049337. Homo sapiens gluc...[gi:14768486] [Related Sequences](#), [Protein](#), [Taxonomy](#), [LinkOut](#)

LOCUS XM_049337 2631 bp mRNA linear PRI 07-FEB-2002
 DEFINITION Homo sapiens glucose-6-phosphate dehydrogenase (G6PD), mRNA.
 ACCESSION XM_049337
 VERSION XM_049337.1 GI:14768486

G6PD

KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2631)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2002) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was
 predicted from NCBI contig NT_025965 by automated computational
 analysis using gene prediction method: BLAST. -Also see:-
 Documentation of NCBI's Annotation Process- Evidence Viewer -
 alignments supporting this model.

FEATURES Location/Qualifiers
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 /chromosome="X"
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 /note="G6PD1; Located on Accession NT_025965"
 /db_xref="LocusID:2539"
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FIG. 13 (2/3)

10/510903

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601 ctggccaaga agaagatcta cccaccatc tggtggctgt tccgggatgg ccttctgccc
661 gaaaacacct tcatcatggg ctatgccgtg tcccgcctca cagtggctga catccgcaaa
721 cagagtgagc ccttcttcaa ggccacccca gaggagaagc tcaagctgga ggacttcttt
781 gcccgaact cctatgtggc tggccagtac gatgatgcag cctcctacca gcgcctcaac
841 agccacatgg atgccctcca cctggggtea caggccaacc gcctcttcta cctggccttg
901 ccccgaccg tctacgaggc cgtcaccaag aacattcacg agtcctgcat gagccagata
961 ggctggaacc gcatcatcgt ggagaagccc ttcgggaggg acctgcagag ctctgaccgg

```

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FIG. 13 (3/3)

1021 ctgtccaacc acatctcctc cctgttccgt gaggaccaga tctaccgcat cgaccactac
1081 ctgggcaagg agatggtgca gaacctcatg gtgctgagat ttgccaacag gatcttcggc
1141 cccatctgga accgggacaa catcgctgc gttatctca ccttcaagga gccctttggc
1201 actgagggtc gcgggggcta ttctgatgaa ttgggatca tccgggacgt gatgcagaac
1261 cacctactgc agatgctgtg tctggtggcc atggagaagc ccgcctccac caactcagat
1321 gacgtccgtg atgagaaggc caaggtgttg aaatgcatct cagaggtgca ggccaacaat
1381 gtggtcctgg gccagtacgt ggggaacccc gatggagagg gcgaggccac caaagggtag
1441 ctggacgacc ccacggtgcc ccgcgggtcc accaccgcca cttttgcagc cgtcgtcctc
1501 tatgtggaga atgagaggtg ggatggggtg cccttcaccc tgcgctgcgg caaggccctg
1561 aacgagcgca aggccgaggt gaggctgcag ttccatgatg tggccggcga catcttccac
1621 cagcagtgca agcgcaacga gctggtgatc cgcgtgcagc ccaacgaggc cgtgtacacc
1681 aagatgatga ccaagaagcc gggcatgttc ttcaaccccg aggagtcgga gctggacctg
1741 acctacggca acagatacaa gaacgtgaag ctccctgacg cctacgagcg cctcatcctg
1801 gacgtcttct gcgggagcca gatgcacttc gtgcgcagcg acgagctccg tgaggcctgg
1861 cgtattttca cccactgct gcaccagatt gagctggaga agcccaagcc catccccat
1921 atttatggca gccgaggccc cacggaggca gacgagctga tgaagagagt gggtttccag
1981 tatgagggca cctacaagtg ggtgaacccc cacaagctct gagecctggg caccacctc
2041 cacccccgc accgccaccc tccttcccgc cgcgcgacc cgagtcggga ggactccggg
2101 accattgacc tcagctgcac attcctggcc ccgggctctg gccaccctgg cccgcccctc
2161 gctgctgcta ctaccgagc ccagctacat tcctcagctg ccaagcactc gagaccatcc
2221 tggccccctc agaccctgcc tgagcccagg agctgagtca cctcctccac tactccagc
2281 ccaacagaag gaaggaggag ggcgccatt cgtctgtccc agagcttatt ggccactggg
2341 tctcactcct gaggggggcc aggggtggag ggagggacaa gggggaggaa aggggcgagc
2401 acccacgtga gagaatctgc ctgtggcctt gccgcgagc ctcagtgcca cttgacattc
2461 cttgtcacca gcaacatctc gagccccctg gatgtccct gtcccaccaa ctctgcactc
2521 catggccacc ccgtgccacc cgtaggcagc ctctctgcta taagaaaagc agacgcagca
2581 gctgggaccc ctcccaacct caatgccctg ccattaaatc cgcaaacagc c

//

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FIG. 14 (1/2)



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 ☐ Structure
 ☐ PopSet
 ☐ Taxonomy
 ☐ OMIM
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1: XM_049047[gi:14759750]

LOCUS XM_049047 1564 bp mRNA linear PRI 16-JUL-2001
 DEFINITION Homo sapiens proliferation-associated 2G4, 38kD (PA2G4), mRNA.
 ACCESSION XM_049047
 VERSION XM_049047.1 GI:14759750
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1564)
 AUTHORS NCBI Annotation Project.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUL-2001) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

HCDR-3

FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="12"
 gene 1..1564
 /gene="PA2G4"
 /db_xref="LocusID:5036"
 /db_xref="MIM:602145"
 CDS 120..1304
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 /codon_start=1
 /product="proliferation-associated 2G4, 38kD"
 /protein_id="XP_049047.1"
 /db_xref="GI:14759751"
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 NQNTQVTEAWNKVAFSNCPTIEGMLSHQLKQHVIDGEKTI IQNPTDQKKDHEKAEF
 EVHEVYAVDVLVSSGEGKAKDAGQRTTIYKRDPKQYGLKMKTSRAFFSEVERRFDAM
 PFTLRAFEDKKARMGVVECAKHELLQPFNVLYEKEGEFVAQFKFTVLLMPNGPMRIT
 SGPFEPLDYKSEMEVQDAELKALLQSSASRKTQKKKKKASKTAENATSGETLEENEA
 GD"

BASE COUNT 455 a 365 c 413 g 331 t
 ORIGIN

```

1  ctttcgctcg ccctctctc gaggatcgag gggactctga ccacagcctg tggctgggaa
61  gggagacaga ggcggcggcg gctcagggga aacgaggctg cagtgggtgg agtaggaaga
121  tgtcggggcg ggacgagcaa caggagcaaa ctatcgctga ggacctggtc gtgaccaagt
181  ataagatggg gggcgacatc gccaacaggg tacttcggtc cttgggtggaa gcatctagct
241  cagggtgtgtc ggtactgagc ctgtgtgaga aagggtgatc catgattatg gaagaaacag
301  ggaaaatctt caagaaagaa aaggaaatga agaaaggatg tgcttttccc accagcattt
361  cggtaaataa ctgtgtatgt cacttctccc ctttgaagag cgaccaggat tatattctca
421  aggaagggtga cttggtaaaa attgaccttg ggggccatgt ggatggcttc atcgctaagt
  
```


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FIG. 14 (2/2)

```
481 tagctcacac ttttgtggtt gatgtagctc aggggaccca agtaacaggg aggaaagcag
541 atgttattaa ggcagctcac ctttgtgctg aagctgccct acgcctgggc aaacctggaa
601 atcagaacac acaagtgaca gaagcctgga acaaagttgc ccactcattt aactgcacgc
661 caatagaagg tatgctgtca caccagttga agcagcatgt catcgatgga gaaaaaacca
721 ttatccagaa tcccacagac cagcagaaga aggaccatga aaaagctgaa tttgaggtag
781 atgaagtata tgctgtggat gttctcgtca gctcaggaga gggcaaggcc aaggatgcag
841 gacagagAAC cactatttac aaacgagacc cctctaaaca gtatggactg aaaatgaaaa
901 cttcacgtgc cttcttcagt gaggtggaaa ggcgttttga tgccatgccg tttactttaa
961 gagcatttga agatgagaag aaggctcgga tgggtgtggt ggagtgcgcc aaacatgaac
1021 tgctgcaacc atttaatgtt ctctatgaga aggagggtga atttggtgcc cagttaaata
1081 ttacagttct gctcatgccc aatggcccca tgcggataac cagtgggtccc ttcgagcctg
1141 acctctacaa gtctgagatg gaggtccagg atgcagagct aaaggccctc ctccagagtt
1201 ctgcaagtcg aaaaaccag aaaaagaaaa aaaagaaggc ctccaagact gcagagaatg
1261 ccaccagtgg ggaaacatta gaagaaaatg aagctgggga ctgagggtggg tcccatctcc
1321 ccagcttgct gctcctgcct catccccttc ccaccaaacc ccagactctg tgaagtgcag
1381 ttctttctcca cctaggaccg ccagcagagc ggggggatct ccctgcccc accccagttc
1441 cccaaccac tcccttccaa caacaaccag ctccaactga ctctggtctt gggagggtgag
1501 gcttcccaac cacggaagac tacttttaaat gaaaaaaaga aattgaataa taaaatcagg
1561 agtc
```

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FIG. 15 (1/2)

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1: XM_052326[gi:14748477]

LOCUS XM_052326 3273 bp mRNA linear PRI 16-JUL-2001
DEFINITION Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (DDX21), mRNA.

ACCESSION XM_052326
VERSION XM_052326.1 GI:14748477

DDX21

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3273)

AUTHORS NCBI Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (12-JUL-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

FEATURES

source

Location/Qualifiers

1..3273

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="10"

gene

1..3273

/gene="DDX21"

/note="GURDB; RH-II/GU"

/db_xref="LocusID:9188"

CDS

35..1711

/gene="DDX21"

/codon_start=1

/product="DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21"

/protein_id="XP_052326.1"

/db_xref="GI:14748478"

/translation="MPGKLRS DAGLES DTAMKKGETLRKQTEEEKKKPKSKDKTEEI

AEEEEETVFPKAKQVKKKAEPSEVDMNSPKSKKAKKKEEPSQNDISP KTKSLRKKKEPI

EKKVVSSTKKVTKNEEPSEEEIDAPKPKMKKKEKEMNGETREKSPKLKNGFPHPEPD

CNPSEAAASEESNSEIEQEIPVEQKEGAFSNFPISEETIKLLKGRGVTFLFPIQAKTFH

HVYSGKDLIAQARTGTGKTFSFAIPLIEKLHGELQDRKGRAPQVLVLAPTRELANQV

SKDFSDITKKLSVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLTKLK

HVVLDDEVQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFSATCPHWVFNVAKKYMK

TYEQVDLIGKKTQKTAITVEHLAIKCHWTQRAAVIGDVIRVYSGHQGRITIIFCETKKE

AQELSQNSAIKQDAQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVDL

VIQSSPPKGCRLVHSSIRADRQSWKDGGVHLLLSAQGRISVSTSGAKSGN"

BASE COUNT 1068 a 603 c 773 g 829 t

ORIGIN

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1 gaagaccggt cggcctgggc aacctgcgct gaagatgccg ggaaaactcc gtagtgacgc
61 tggtttggaa tcagacaccg caatgaaaaa aggggagaca ctgcgaaaagc aaaccgagga
121 gaaagagaaa aaagagaagc caaaatctga taagactgaa gagatagcag aagaggaaga
181 aactgttttc cccaaagcta aacaagttaa aaagaaagca gaggccttctg aagttgacat
241 gaattctcct aaatccaaaa aggcaaaaaa gaaagaggag ccatctcaaa atgacatttc
```

FIG. 15 (2/2)

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301 tcctaaaacc aaaagtttga gaaagaaaaa ggagcccatc ga'aa'gaa'g'gggtttcttc
 361 taaaaccaa aaagtgcacaa aaaatgagga gccttctgag gaagaaatag atgctcctaa
 421 gcccaagaag atgaagaaag aaaaggaaat gaatggagaa actagagaga aaagcccaa
 481 actgaagaat ggatttcctc atcctgaacc ggactgtaac cccagtgaag ctgccagtga
 541 agaaagtaac agtgagatag agcaggaaat acctgtggaa caaaaagaag gcgctttctc
 601 taattttccc atatctgaag aaactattaa acttctcaaa ggccgaggag tgaccttctc
 661 atttctata caagcaaaga cattccatca tgtttacagc gggaaggact taattgcaca
 721 ggcacggaca ggaactggga agacattctc ctttgccatc ctttgattg agaaacttca
 781 tggggaactg caagacagga agagaggccg tggccctcag gtactggttc ttgcacctac
 841 aagagagttg gcaaatacaag taagcaaaga ctacagtgc atcacaaaaa agctgtcagt
 901 ggcttggttt tatggtggaa ctccctatgg aggtcaattt gaacgcata ggaatgggat
 961 tgatatcctg gttggaacac caggctgat caaagaccac atacagaatg gcaaactaga
 1021 tctcaccaa ctttaagcatg ttgtcctgga tgaagtggac cagatgttg atatgggatt
 1081 tgctgatcaa gtggaagaga ttttaagtgt ggcatacaag aaagattctg aagacaatcc
 1141 ccaaacttg ctttttctg caacttgccc tcattgggta tttaatgtg ccaagaaata
 1201 catgaaatct acatatgaac aggtggacct gattggtaaa aagactcaga aaacggcaat
 1261 aactgtggag catctggcta ttaagtcca ctggactcag agggcagcag ttattgggga
 1321 tgtcatccga gtatatagt gtcatacagg acgcactatc atcttttctg aaaccaagaa
 1381 agaagccag gagctgtccc agaattcagc tataaagcag gatgctcagt ccttgcatgg
 1441 agacattcca cagaagcaaa gggaaatcac cctgaaagg tttagaaatg gtatgtttgg
 1501 agttttggtg gcaaccaatg ttgctgcacg tgggttagac atccctgagg ttgatttgg
 1561 tatacaaagc tctccaccaa agggatgtag agtccatcat tcacgatcc gggcggacag
 1621 gcagagctgg aaggacgggg gtgtgcacat gcttttatca gcacaaggaa gaatatcagt
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 1741 cagaataat aaaagcttcc agcaaagatg ccatcaggct tttggattcc gtgcctcca
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 1861 aagctctggc agcagcactg gcccatattt cagggtgccac gtccgtagac cagcgtcct
 1921 tgatcaactc aaatgtgggt tttgtgacca tgatcttgca gtgctcaatt gaaatgccaa
 1981 atattagtta tgcttggaag gaacttaaag agcagctggg cgaggagatt gattccaaag
 2041 tgaagggaat ggtttttctc aaaggaaagc tgggtgttg ctttgatgta cctaccgat
 2101 cagtaacaga aatacaggag aaatggcatg attcacgacg ctggcagctc tctgtggcca
 2161 cagagcaacc agaactggaa ggaccacggg aagatatagg aggcttcagg ggacagcggg
 2221 aaggcagtcg aggtctcagg ggacagcggg acggaaacag aagattcaga ggacagcggg
 2281 aaggcagtag aggcccgaga ggacagcag caggagggtg caacaaaagt aacagatccc
 2341 aaaacaaagg ccagaagcgg agtttcagta aagcatttgg tcaataatta gaaatagaag
 2401 atttatatag caaaaagaga atgatgtttg gcaatataga actgaacatt atttttcatg
 2461 caaagttaaa agcacattgt gcctcctttt gaccacttgc caagtccctg tctctttcag
 2521 acacagacaa gcttcattta aattatttca tctgatcatt atcatttata actttattgt
 2581 tacttcttca tcagtttttc cttttgaaag gtgtatgaat tcattacttt tttattctaa
 2641 tgtattatct gtagattaga agataaaatc aagcatgtat ctgcctatac tttgtgagtt
 2701 cacctgtcct tatactcaaa agtgtccctt aatagtgtcc ttccctgaaa taaataccta
 2761 agggagtgtg acagtctctg gaggaccact ttgagccttt ggaagttaag gtttctcag
 2821 ccacctgccg aacagtttct catgtgttcc tattatttgt ctactgagac ttaatactga
 2881 gcaatgtttt gaaacaagat ttcaaactaa tctgggttgt aatacagttt ataccagtgt
 2941 atgctctaga cttggaagat gtagtatgtt tgatgtggat tacctatact tatgttcgtt
 3001 ttgatacatt tttagcttct cattataagg tgattcatgc tttagtgaat tcttcataga
 3061 tagtatatat aaaagtacat tttaatagaa agccagggtt ttaagggaatt tcacatgtat
 3121 aagggtggct catagcttta tttgtaagta ggctggataa atggtgctta aatggtaatg
 3181 tactccactt ctccctattg gaagattaac attatttacc aagaaggact taaggagta
 3241 gggggcgcag attagcattg ctcaagagta tgt

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FIG. 16 (1/2)



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1: XM_030607[gi:14786409]

LOCUS XM_030607 2005 bp mRNA linear PRI 16-OCT-2001

DEFINITION Homo sapiens serine/threonine kinase 15 (STK15), mRNA.

ACCESSION XM_030607

VERSION XM_030607.1 GI:14786409

KEYWORDS

ARK2

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2005)

AUTHORS NCBI Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

FEATURES

Location/Qualifiers

source

 1..2005
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 /db_xref="taxon:9606"
 /chromosome="20"

gene

 1..2005
 /gene="STK15"
 /note="BTAK; Located on Accession NT_011362"
 /db_xref="LocusID:8465"
 /db_xref="MIM:603072"

CDS

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 /note="Located on Accession NT_011362"
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 PSAPENNPEEELASKQKNEESKKRQWALEDFEIGRPLGKGFVNLAREKQSKFILA
 LKVLFFKAQLEKAGVEHQLRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTV
 YRELQKLSKFDEQRTATYITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFG
 WSVHAPSSRRITLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTY
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 CQNKESASKQS"

misc feature

 422..1174
 /note="S_TKc; Region: Serine/Threonine protein kinases,
 catalytic domain"

misc feature

 422..1174
 /note="pkinase; Region: Protein kinase domain"

misc feature

 425..1162
 /note="TyrKc; Region: Tyrosine kinase, catalytic domain"

BASE COUNT 585 a 434 c 456 g 530 t

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FIG. 16 (2/2)

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1   cttgggtcct tgggtcgcag gcatcatgga cggatctaaa gaaaactgca ttccaggacc
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121 ttgtcagaat ccattacctg taaatagtgg ccaggctcag cgggtcttgt gtccttcaaa
181 ttcttcccag cgcattcctt tgcaagcaca aaagcttgct tccagtcaca agccgggtca
241 gaatcagaag cagaagcaat tgcaggcaac cagtgtacct catcctgtct ccaggccact
301 gaataacacc caaaagagca agcagccccct gccatcggca cctgaaaata atcctgagga
361 ggaactggca tcaaaacaga aaaatgaaga atcaaaaaag aggcagtggg ctttgggaaga
421 ctttgaaatt ggtcgccctc tgggtaaaagg aaagtttggt aatgtttatt tggcaagaga
481 aaagcaaagc aagtttattc tggctcttaa agtgttattt aaagctcagc tggagaaagc
541 cggagtggag catcagctca gaagagaagt agaaatacag tcccaccttc ggcatacctaa
601 tattcttaga ctgtatgggt atttccatga tgctaccaga gtctacctaa ttctggaata
661 tgcaccactt ggaacagttt atagagaact tcagaaactt tcaaagtttg atgagcagag
721 aactgctact tatataacag aattggcaaa tgccctgtct tactgtcatt cgaagagagt
781 tattcataga gacattaagc cagagaactt acttcttgga tcagctggag agcttaaaat
841 tgcagatttt ggggtggtcag tacatgctcc atcttccagg aggaccactc tctgtggcac
901 cctggactac ctgccccctg aaatgattga aggtcggatg catgatgaga aggtggatct
961 ctggagcctt ggagttcttt gctatgaatt tttagttggg aagcctcctt ttgaggcaaa
1021 cacataccaa gagacctaca aaagaatatc acgggttgaa ttcacattcc ctgactttgt
1081 aacagagggg gccaggggacc tcatttcaag actgttgaag cataatccca gccagaggcc
1141 aatgctcaga gaagtacttg aacacccctg gatcacagca aattcatcaa aaccatcaaa
1201 ttgccaaaac aaagaatcag ctagcaaaca gtcttaggaa tcgtgcaggg ggagaaatcc
1261 ttgagccagg gctgccatat aacctgacag gaacatgcta ctgaagttta ttttaccatt
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1441 agccacgaga attgtgtctac ttatactggg tcataatctg gaggcaaggt tcgactgcag
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1621 tcctagtacc tgagtgaagt tgtaacttat tgggttggcg aagcctggtg aagctgttgg
1681 aatgagtatg tgattctttt taagtatgaa aataaagata tatgtacaga cttgtatttt
1741 ttctctgggt gcattccttt aggaatgctg tgtgtctgtc cggcaccctg gtaggcctga
1801 ttgggtttct agtcctcctt aaccacttat ctcccatatg agagtgtgaa aaataggaac
1861 acgtgctcta cctccattta gggatttgct tgggatacag aagaggccat gtgtctcaga
1921 gctgttaagg gcttattttt ttaaaacatt ggagtcatag catgtgtgta aactttaaat
1981 atgcaaataa ataagtatct atgtc

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FIG. 17 (1/2)

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1: BC008442. Homo sapiens,
Sim...[gi:14250074]

Related Sequences, Protein, Taxonomy, UniSTS,
LinkOut

LOCUS BC008442 1584 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, Similar to transmembrane 4 superfamily member 1,
clone MGC:14656 IMAGE:4101110, mRNA, complete:cds.
ACCESSION BC008442
VERSION BC008442.1 GI:14250074
KEYWORDS MGC. TM4 SF1
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1584)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 21 Row: 1 Column: 7

This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES

source

Location/Qualifiers

1..1584

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="MGC:14656 IMAGE:4101110"

/tissue_type="Bone marrow, chronic myelogenous leukemia"

/clone_lib="NIH_MGC_54"

/lab_host="DH10B"

/note="Vector: pDNR-LIB"

CDS

102..710

10/510903

FIG. 17 (2/2)

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/db_xref="GI:14250075"
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RFVWFFSGIVGGLLMLLPAFVFIGLEQDDCCGCCGHENCGKRCAMLSSVLAALIGIA
GSGYCVIVAALGLAEGPLCLDSLQWNYTFASTEGQYLLDTSTWSECTEPKHIVEWNV
SLFSILLALGGIEFILCLIQVINGVLGGICGFCCSHQQQYDC"

```

BASE COUNT	460 a	311 c	337 g	476 t			
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	61	ctgaagacaa	agagaagg	gagaaaacct	agcagaccac	catgtgctat	gggaagtgtg
	121	cacgatgcat	cggacattct	ctggtggggc	tgcctctcct	gtgcatcgcg	gctaataattt
	181	tgctttactt	tcccaatggg	gaaacaaagt	atgcctccga	aaaccacctc	agccgcttcg
	241	tgtggttctt	ttctggcatc	gtaggagggtg	gcctgctgat	gctcctgcca	gcatttgtct
	301	tcattgggct	ggaacaggat	gactgctgtg	gctgctgtgg	ccatgaaaac	tgtggcaaac
	361	gatgtgcat	gctttcttct	gtattggctg	ctctcattgg	aattgcagga	tctggctact
	421	gtgtcattgt	ggcagccctt	ggcttagcag	aaggaccact	atgtcttgat	tccctcggcc
	481	agtggaaacta	cacctttgcc	agcaccgagg	gccagtacct	tctggatacc	tccacatggg
	541	ccgagtgcac	tgaacccaag	cacattgtgg	aatggaaatgt	atctctgttt	tctatcctct
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	661	gaggcatatg	tggcttttgc	tgtctcacc	aacagcaata	tgactgctaa	aagaaccaac
	721	ccaggacaga	gccacaatct	tcctctatct	cattgtaatt	tatatatttc	acttgtattc
	781	atgtgtaaaa	ctttgtatta	gtgtaacata	ctccccacag	tctactttta	caaacgcctg
	841	taaagactgg	catcttcaca	ggatgtcagt	gtttaaattt	agtaaaacttc	ttttttgttt
	901	gtttatttgt	ttttgttttt	tttttaggaa	tgaggaaaca	aaccaccctc	tgggggtagt
	961	ttacagactg	agtgcacagta	ctcagtatat	ctgagataaa	ctctataatg	ttttggataa
	1021	aaataacatt	ccaatcacta	ttgtatatat	gtgcatgtat	tttttaaat	aaagatgtct
	1081	agttgctttt	tataagacca	agaaggagaa	aatccgacaa	cctggaaaga	ttttgttttt
	1141	cactgcttgt	atgatgtttc	ccattcatac	acctataaat	ctctaacaag	aggccctttg
	1201	aactgccttg	tgttctgtga	gaaacaaata	tttacttaga	gtggaaggac	tgattgagaa
	1261	tgttccaatc	caaataaatg	catcacaact	tacaatgctg	ctcattgttg	tgagtactat
	1321	gagattcaaa	tttttctaac	atatggaaa	ccttttgtcc	tccaaagatg	agtactaggg
	1381	atcatgtgtt	taaaaaaaag	aaaggctacg	atgactgggc	aagaagaaag	atgggaaact
	1441	gaataaagca	gttgatcagc	atcattggaa	catggggacg	agtgcaggca	ggaggaccac
	1501	gaggaaatac	cctcaaaaact	aacttgttta	caacaaaata	aagtattcac	tacgaaaaaa
	1561	aaaaaaaaaa	aaaaaaaaaa	aaaa			

//

Revised: October 24, 2001.

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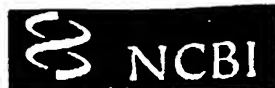


FIG. 18 (1/2)

10/510903
Nucleotide

PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

B

Search for

Limits

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History

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Details

Display

1: XM_027538[gi:14768648]

LOCUS XM_027538 1025 bp mRNA linear PRI 16-JUL-2001
 DEFINITION Homo sapiens excision repair cross-complementing rodent repair
 deficiency, complementation group 1 (includes overlapping antisense
 sequence) (ERCC1), mRNA.

ACCESSION XM_027538
 VERSION XM_027538.1 GI:14768648

ERCC1

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1025)

AUTHORS

NCBI Annotation Project.

TITLE

Direct Submission

JOURNAL

Submitted (12-JUL-2001) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA

FEATURES

Location/Qualifiers

source

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 /db_xref="taxon:9606"
 /chromosome="19"

gene

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 /gene="ERCC1"
 /note="UV20"
 /db_xref="LocusID:2067"
 /db_xref="MIM:126380"

CDS

63..956
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 repair deficiency, complementation group 1 (includes
 overlapping antisense sequence)"
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 VSPRQRGNPVLKFVRNVPWEFGDVIPDYVLGQSTCALFLSLRYHNLHPDYIHGRLQSL
 GKNFALRVLLVQVDVKDPQQALKELAKMCILADCTLILAWSPEEAGRYLETYKAYEQK
 PADLLMEKLEQDFVSRVTECLTVKSVNKTDSTLLTTFGSLEQLIAASREDLALCPG
 LGPQKARRLFDVLHEPFLKVP"

BASE COUNT 234 a 326 c 289 g 176 t

ORIGIN

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61 agatggaccc tgggaaggac aaagaggggg tgcccagcc ctcagggccg ccagcaagga
121 agaaatttgt gatacccctc gacgaggatg aggtccctcc tggagtggcc aagcccttat
181 tccgatctac acagagcctt cccactgtgg acacctcggc ccaggcggcc cctcagacct
241 acgccgaata tgccatctca cagcctctgg aaggggctgg ggccacgtgc cccacagggt

```


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FIG. 18 (2/2)

```
301 cagagcccct ggcaggagag acgcccaccc aggccctgaa acccggggga aaatccaaca
361 gcatcattgt gagccctcgg cagaggggca atcccgtact gaagtctcgt cgcaatgtgc
421 cctgggaatt tggcgacgta attcccgact atgtgctggg ccagagcacc tgtgccctgt
481 tcctcagcct ccgctaccac aacctgcacc cagactacat ccatgggcgg ctgcagagcc
541 tggggaagaa cttcgccttg cgggtcctgc ttgtccagggt ggatgtgaaa gatccccagc
601 aggccctcaa ggagctggct aagatgtgta tcctggccga ctgcacattg atcctcgctt
661 ggagccccga ggaagctggg cggtagctgg agacctaca ggcctatgag cagaaaccag
721 cggacctcct gatggagaag ctagagcagg acttcgtctc ccgggtgact gaatgtctga
781 ccaccgtgaa gtcagtcaac aaaacggaca gtcagacctt cctgaccaca tttggatctc
841 tggaacagct catcgccgca tcaagagaag atctggcctt atgcccaggc ctgggccttc
901 agaaagcccg gaggctgttt gatgtcctgc acgagccctt cttgaaagta ccctgatgac
961 ccagctgcc aaggaaaccc ccagtgtaat aataaatcgt cctcccaggc caggctcctg
1021 ctggc
```

//

Revised: October 24, 2001.

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G2-2F3 // Fanconi Anemia Group A (FANCA)

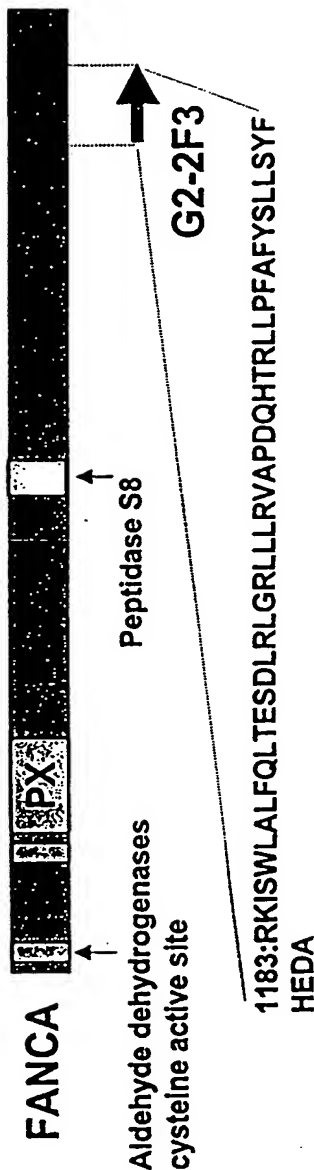
The G2-2F3 sequence is identical to Fanconi Anemia Group A,

FANCA, 1340aa

Orientation : Sense

FKBP-type peptidyl-prolyl
cis-trans isomerase signature 1

FANCA



Pfam HMM search was done at the Washington University web site

Aldehyde dehydrogenases cysteine active site (3-14): It is found in a nuclear protein associated with cell proliferation

FKBP-type peptidyl-prolyl cis-trans isomerase signature 1(159-175): One of two signature patterns for FKBP

PX(189-320): Novel domains in NADPH oxidase subunits, sorting nexins, and PI3-kinases: binding partners of SH3 domains?

PeptidaseS8(660-688): Subtilase family motif

FIG. 19

10/510903

Cell Tracker Analysis of G2-2F3 (The Fragment of FANCA)-Infected A549.tTA Cells

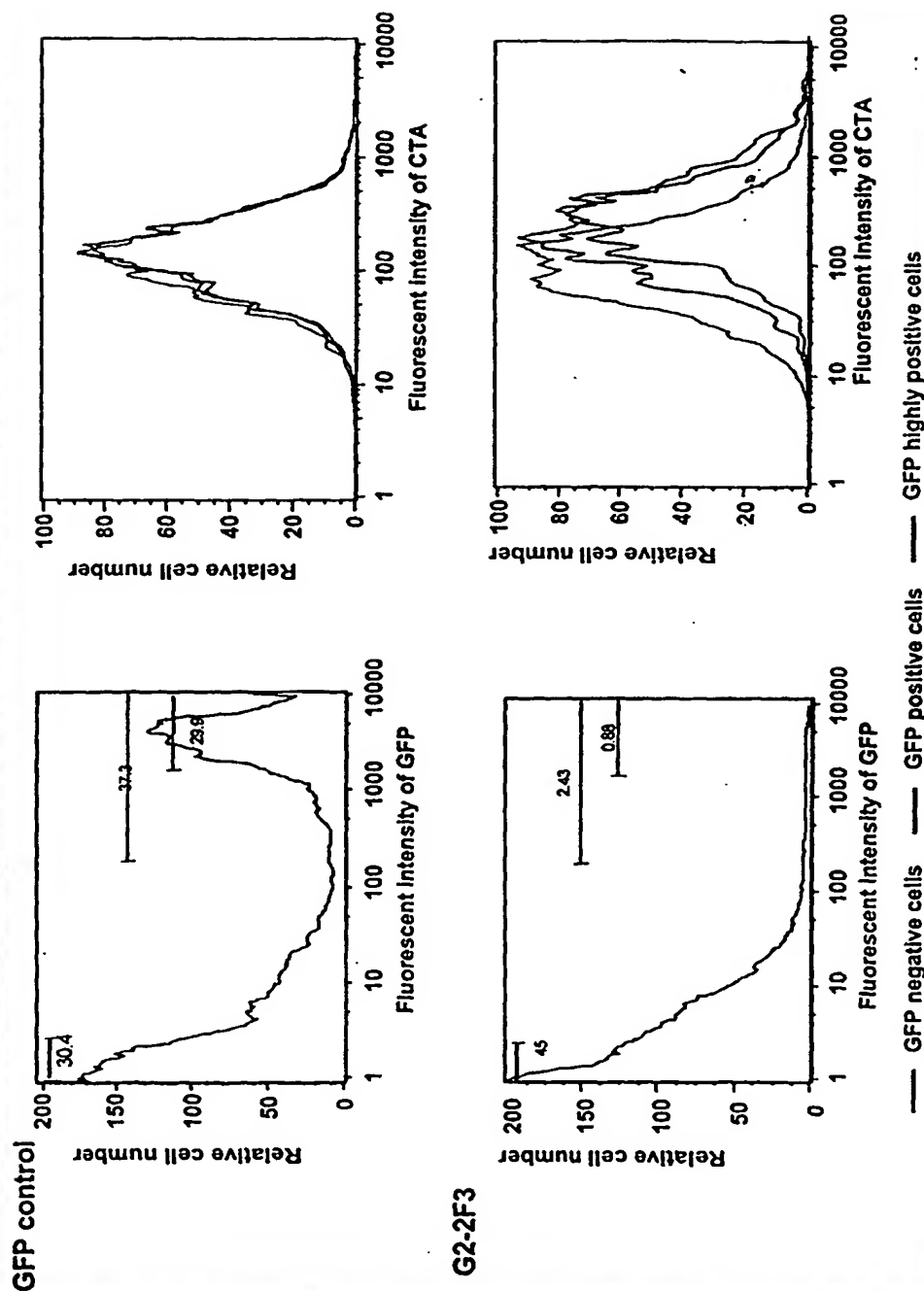
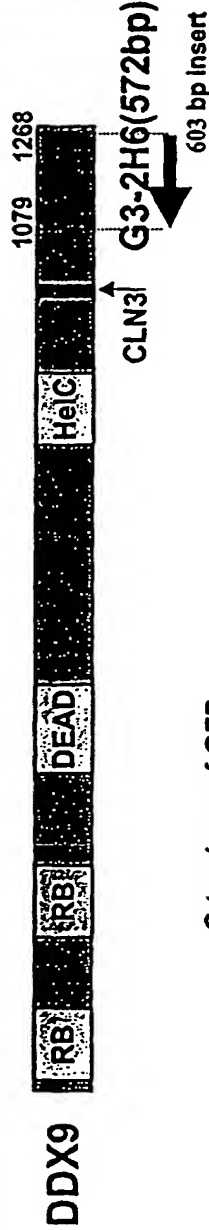


FIG. 20

10/510903

G3-2H6 // DEAD/H Box Polypeptide 9 (DDX9)

The G3-2H6 sequence is identical to DEAD/H box polypeptide 9 (DDX9), 1279aa
Orientation: Antisense



C-terminus of GFP

GAGTTCGIGACCGCGCGGATCCTCTGGCATGGACGAGCTGTACAAGGAGAGGCC
GCCAAGGCC
E F V T A G I T L G M D E L Y K E E A A K A
GGTGGCAGCGGTGGCTCCAGTGTGCTGGAAAGCGCCACCTCCTCTCCCTGTCCAAAGTA
GCCAGTTCC
G G S G S V L E S A T S S L S K V A S S
ATAGGCCCCCTACCACCTCCTCGCTGGAATCCCCCAGATCCTCTGTAGCCTCCACTAGGC
CCTCTGTA
I G P P T T S S L E S P R S S V A S T R P S V
GTCTCCTCCAGAGTTGCCCTCTAAAGCCACCTCGGGAGACTCCTCTATAGCCTCCACCAACA
CCTGCACC
V S S R V A S K A T S G D S I A S T N T C T
ATATCCTGCCGAAAGGAGTTGGCGCTGCCACCAATAGCCTCCGCTACCATAGCCTCCACTG
CTATAGCC
I S C P K G V G A T I A S A T I A S T A I A
ACCGCATAGCCTCCACCACTGTAACCTAGAACCTCCCTTCTATATCCGCTTCCATTGTCGTA
TGGGCGCC
RE(488, 181-250): Double-stranded RNA binding motif
LA(508, 183-210): RNA binding motif
DEAD(488-568): DEAD box polypeptide domain
HEC(679-679): Helicase conserved C-terminal domain
= BstXI linker
GATAGCA

FIG. 21

Cell Tracker Analysis of G3-2H6 (The Antisense Fragment of DDX9)-Infected A549.tTA Cells

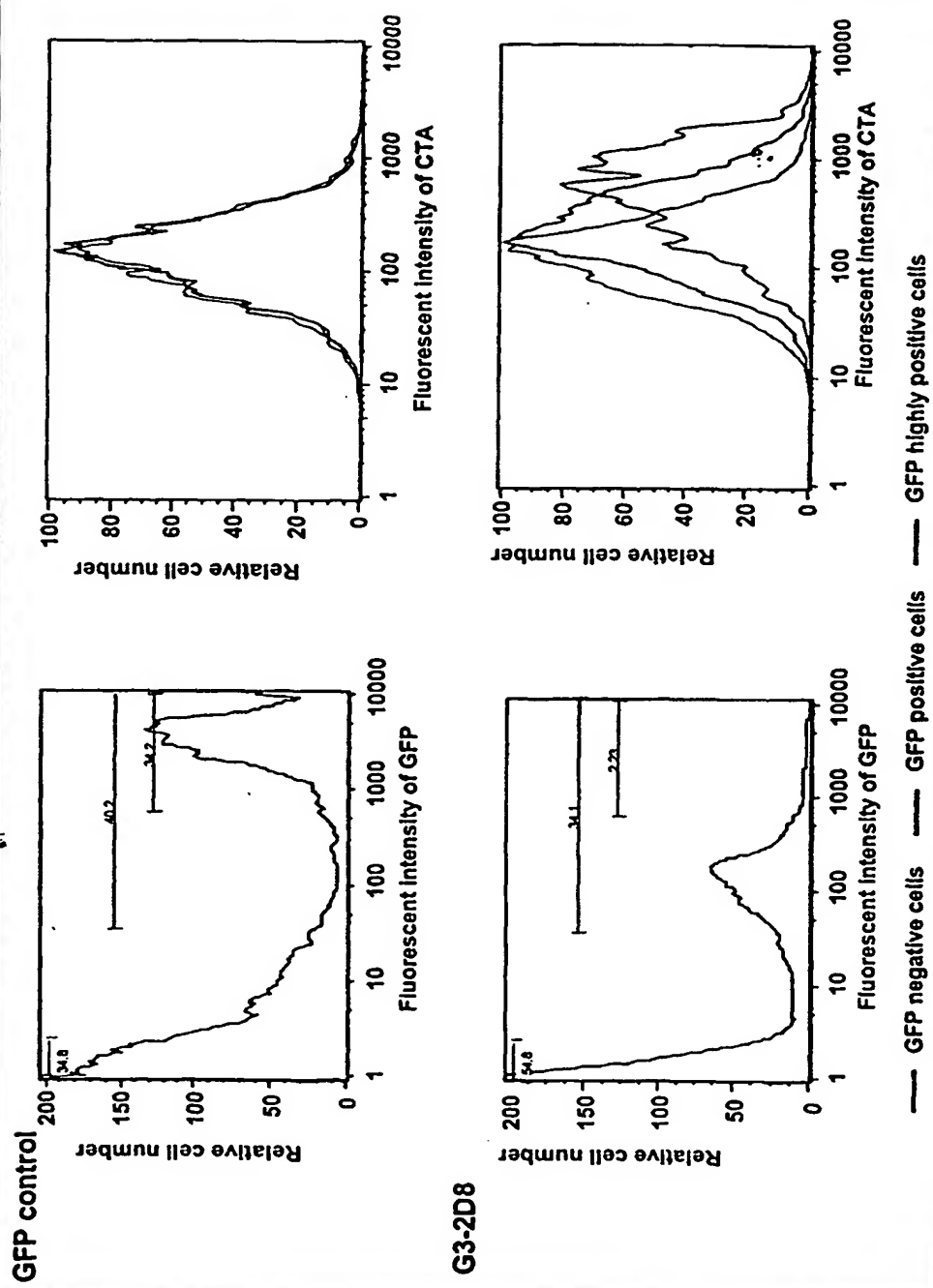


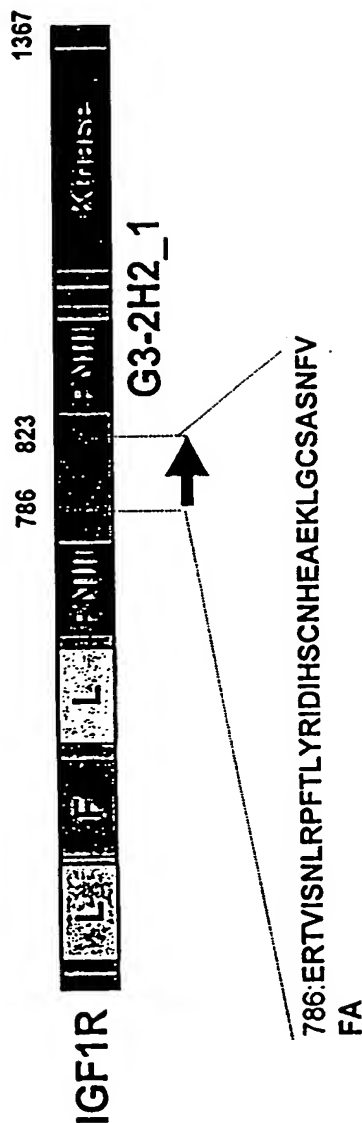
FIG. 22

10/510903

G3-2H2_1/Insulin-like Growth Factor 1 Receptor (IGF1R)

The G3-2H2_1 sequence is identical to Insulin-like growth factor 1 receptor (IGF1R)

Orientation: Sense



Leader sequence (1-30)
 L (51-172, 352-472): Receptor L domain, the L domains from insulin-like growth factor receptors make up the bilobal ligand binding site.
 F (175-333): Furin-like cysteine rich region, which involves receptor aggregation
 FNIII(489-587, 835-917): Fibronectin type III domain, the majority of which are involved in cell surface binding in some manner, or are receptor protein tyrosine kinases, or cytokine receptors.
 Transmembrane (936-958)
 Kinase(999-1266): Protein tyrosine kinase catalytic domain

FIG. 23

Cell Tracker Analysis of G3-2H2_1 (The Fragment of IGF1R)-Infected A549.tTA Cells

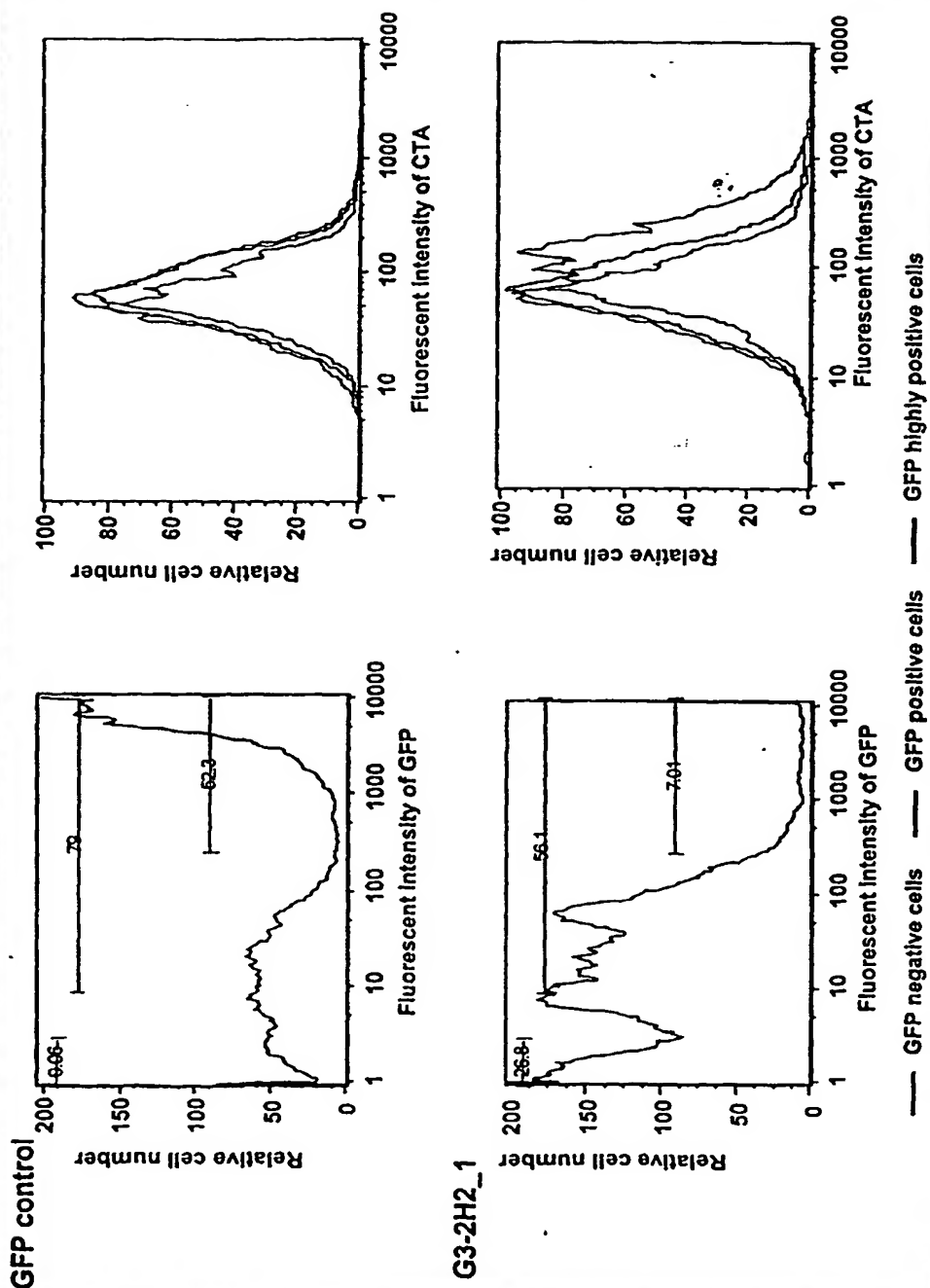


FIG. 24

FIG. 25

Cell Tracker Analysis of G3-2G2/2H2 (The Antisense Fragment of UBE2V1)-Infected A549.tTA Cells

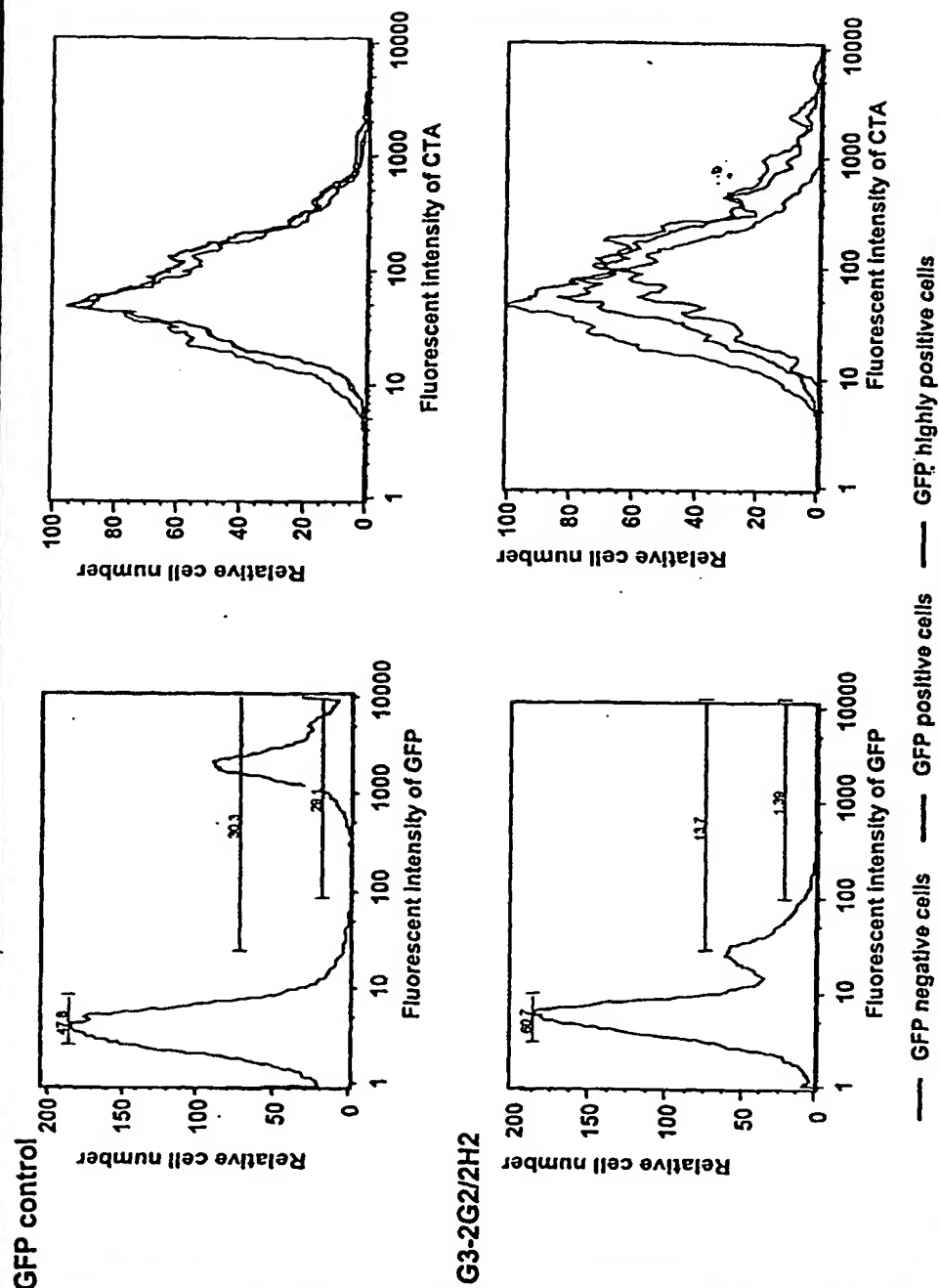


FIG. 26

G3-2G2//2H2 inhibits all UBE2V1 isoforms,

UBE2V1 has 4 alternatively spliced UBE2V1 transcripts that encode proteins with the conserved Ubc domain of E2 enzymes and unique N-terminal sequences.

_____GGCAGCCACCAGGGCTGGGAGTAAAGTCCCTCGCAATTTCCGACTGTTGGAGAAGAACTCGAA 84
 _____G-GCAGAGG-GGACGGCAAGT-GGCAGCCAGGGCTCGGAGTAAAGTCCCTCGCAATTTCCGACTGTTGGAGAAGAACTCGAA 85
 GTCACTCTGCACGTAACACATCGATCATCA-CCAGCTCTCCACCAAGAGCC-TACTCTCAAGTCAACAGAGTAAAGTCCCTCGCAATTTCCGACTGTTGGAGAAGC
 AAGCGTCTTACCTGAAGTCAACAAGCAAGTGAAGTGAAGGAAGTCAAGCTAGMAAATTTCACTGCAAGGAGTAAAGTCCCTCGCAATTTCCGACTGTTGGAGAAGC
 _____ATGCGCTCAAGTTCGACAGAGTGTACAGCCCTGGAGTAAAGTCCCTCGCAATTTCCGACTGTTGGAGAAGAACTCGAA 79
 _____CGGTCGGGCTGAGGAGA-AGATGGCGGTCTCCACGAGTAAAGTCCCTCGTAAATTTTCGCTGTTGGAGAAGAACTCGAA 81

[illegible]

CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGAGC-----233
CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGAGCCTTGTGA285
CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGAGCCTTGTGA137
CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGAGCCTTGTGA384
CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGAGCCTTGTGA259
CGAATATACAGCCTTAAATAGAATGTGGACCTAAATACCGAAGCCTCTCGTCAGT281

FIG. 27

FIG. 28 (1/2)

10/510903

SEQ ID NO:29

Size: 181

DNA FANCA

CCAGTGTGCTGGAAAGGAGGAAGATATCCTGGCTGGCACTCTTTCAGTTGACAGAGAGTGACCTCAGGCTGGGGC
GGCTCCTCCTCCGTGTGGCCCCGGATCAGCACACCAGGCTGCTGCCTTTTCGCTTTTTACAGTCTTCTCTCCTACT
TCCATGAAGACGCGGCTTTCCAGCACAGTGG

SEQ ID NO:30

Size: 603

DNA DDX9

CCAGTGTGCTGGAAAGCGCCACCTCCTCTTCCCTGTCCAAAGTAGCCAGTTCCATAGGCCCCCTACCACCWCCT
CGCTGGAATCCCCCAGATCCTCTGTAGCCTCCACTAGGCCCTCTGTAGTCTCCTCCAGAGTTGCCTCTAAAGCCA
CCTCGGGAGACTCCTCTATAGCCTCCACCAACACCTGCACCATATCCTGCCCCGAAAGGAGTTGGCGCTGCCACCA
TAGCCTCCGCTACCATAGCCTCCACTGCTATAGCCACCGCATAGCCTCCACCACTGTAAGTAAACCTCCCTTC
TATATCCGCTTCCATTGTCTGTATCGGGCCATCTTGGGAGGACGTGGACCATCTCCATGCCGTGTACTGCCAATCA
TAAGGTTGATACCAGCAGCTGAGGGTCTAGAGATCTGACGGATCATGTTTCAGCATACGTTTCATTTACGGGGTCCA
ACTGGCTGATGATAGCAGGTTGTTTGGTTACTTCAACAACCAAAGCCTCCATGGCTGCCCGGAGACCAGTGATAC
AGGCAGCAGCTTCATGAGATATTTGCAGTTTAATCCAGTCATCTACAAGCACAAATCTGCCCCACTTTCCAGCACAG
TGG

SEQ ID NO:31

Size: 145

DNA IGF1R

CCAGTGTGTTGGAAAGGGAGAGAACTGTCATTTCTAACCTTCGGCCTTTCACATTGTACCGCATCGATATCCACA
GCTGCAACCACGAGGCTGAGAAGCTGGGCTGCAGCGCCTCCAACCTTCGTCTTTGCTTTCCAGCACAGTGG

SEQ ID NO:32

Size: 269

DNA UBEV2V1

CCAGTGTGCTGGAAAGGTGCTTCTGGGTATTTAGGTCCACATTCTATTTTAAGGCTGTATATTCGGTTTTTCATAA
ATTGTTCTTGGAGGCCCAATTATCATCCCTGTCCATCTTGTAAGATGTCATGTCTTCGTCATCTTCTAGACCCCA
GCTAACTGTGCCATCTCCTACTCCTTTCTGGCCTTCTTCGAGATTCTTCCAACAGTCGGAAATTGCGAGGGACTT
TATACATCCCAGCCCCGTGGTGGCTGCCCTTTCCAGCACACTGG

SEQ ID NO:33

Size: 499

DNA aldehyde dehydrogenase

CCAGTGTGCTGGAAAGGAGCAAACCTCCTCTCACTGCTCTCCACGTGGCATCTTTAATAAAAAGAGGCAGGGTTTCC
TCCTGGAGTAGTGAATATTGTTCCCTGGTTATGGGCCTACAGCAGGGGCAGCCATTCTTCTCACATGGATATAGA
CAAAGTAGCCTTCACAGGATCAACAGAGGTTGGCAAGTTGATCAAAGAAGCTGCCGGGAAAAGCAATCTGAAGAG
GGTGACCCTGGAGCTTGGAGGAAAAGAGCCCTTGCAATTGTGTTAGCTGATGCCGACTTGGACAATGCTGTTGAATT
TGCACACCATGGGGTATTCTACCACCAGGGCCAGTGTGTATAGCCGCATCCAGGATTTTTGTGGAAGAATCAAT
TTATGATGAGTTTTGTTTGAAGGAGTGTTGAGCGGGCTAAGAACGTATATCCTTGGAAACATCCTCTGACCCAG
GAGTCACTCAAAGGCCCTCAGATTGACAAGGACTTTCCAGACACAGTGG

SEQ ID NO:34

Size: 425

DNA pyruvate kinase

FIG. 28 (2/2)

CCAGTGTGCTGGAAAGGCTGCCACTTCCACCACCTTGCAGATGTTCTTGTAGTCCAGCCACAGGATGTTCTCGT
CACACTTTTCCATGTAGGCGTTATCCAGCGTGATTTTGAGAGTGGCTCCCTTCTTCAGCTCCACCTCTGCAGTGC
CGCTGCCCTTGTATGAGCCCAGTTCCGATCTCAGGTCCCTTTAGTGTCTAGAGCCACAGCAACGGGCCGGTAGAGGA
TGGGGTCAGAAGCAAAAGCTTTCGTGGCTGTGCGCACATATCTTGATGGTCTCCGCATGGTACTCATGATTCCAT
GAGAGAAGTTTCAGACGAGCCACATTCACTCCAGACTAATCATCTCCTTCAACGTCCTCCACTGGATCGGGAAGCT
GGGCCAATGGTACAGATGATGCCAGTGTTCGGGCTTTCCAGCACAGTGG

SEQ ID NO:35

Size:

DNA G6PD

CCAGTGTGCTGGAACTTTCCAGTTCTCCATGGCCACCANACACAGCATCTGCAGTAGGTGGTTCTGCATCACGT
CCCGGATGATCCCAAATTCATCGAAATAGCCCCGCGACCTCAGTGCCAAAGGGCTCCTTGAAGGTGAGGATAA
CGCAGGCGATGTTGTCCCGTTCCANATGGGGCCGAAGATCCTGTTGGCAAATCTCAGCACCATGAGGTTCCTCTT
TCCAGCACAGTGG

10/510903

Dominant Negative Mutants of BAP-1

Point mutants: C91A, H169A- catalytic residues in the protease domain.
(EMBO J. 1997 Jul 1;16(13):3787-96. PMID: 9233788)

CLUSTAL W (1.8) multiple sequence alignment

```

Uch-13      MEGQRWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMDELLSMVPRPVCVALLFPITE
BAP-1      MNKGWLELESDPGLFTLLVEDFGVGK-VQVEEIIY----DLQSKCQGPVYGFIFLQK
           .: ** **:*: : . :*:*:*: ** **:*:*:*: ** **:*:*:*:
Uch-13      KYEVFR--TEEEKIKSQGDVTSSVYFMKQTI↓SNACGTIGLIHAIANNKDMHFESGST
BAP-1      ERRSRKVTSLVDDTSVIDDDIVNNMFFAHQLIPNSCATHALLSVLLNCSS--VDLGPT
           : . * : : . . . :*:*:*:*: * :*:*:*: * :*: * : * :
Uch-13      LKKFLEESVMSPEERARYLENYDAIRVTHETSAHEGQTEAP-----SIDEKVDLHFI
BAP-1      LSRMKDFTKGFSPESKGYAIGNAPELAKAHNSHARPEPRHLPEKQNGLSAVRTMEAFHFV
           *:*: : : :*:*:*: : * :*:*: * : * : * : * :
Uch-13      ALVHVDGHLIELDGRKPPFINHGETS-DETLLEDAIEVCKFMERDPD-----ELRFNAI
BAP-1      SYVPITGRLLFELDGLKVYPIDHGPWGEDEEWTDKARRVIMERIGLATAGEPYHDIRFNL
           : * :*:*:*:*: * :*:*: * : * : * : * : * : * :

```

Bold: Catalytic residue

FIG. 29

RIGEL

10 / 510903

Expression of Bap1 WT and Protease Mutants is Antiproliferative in HeLa Cells

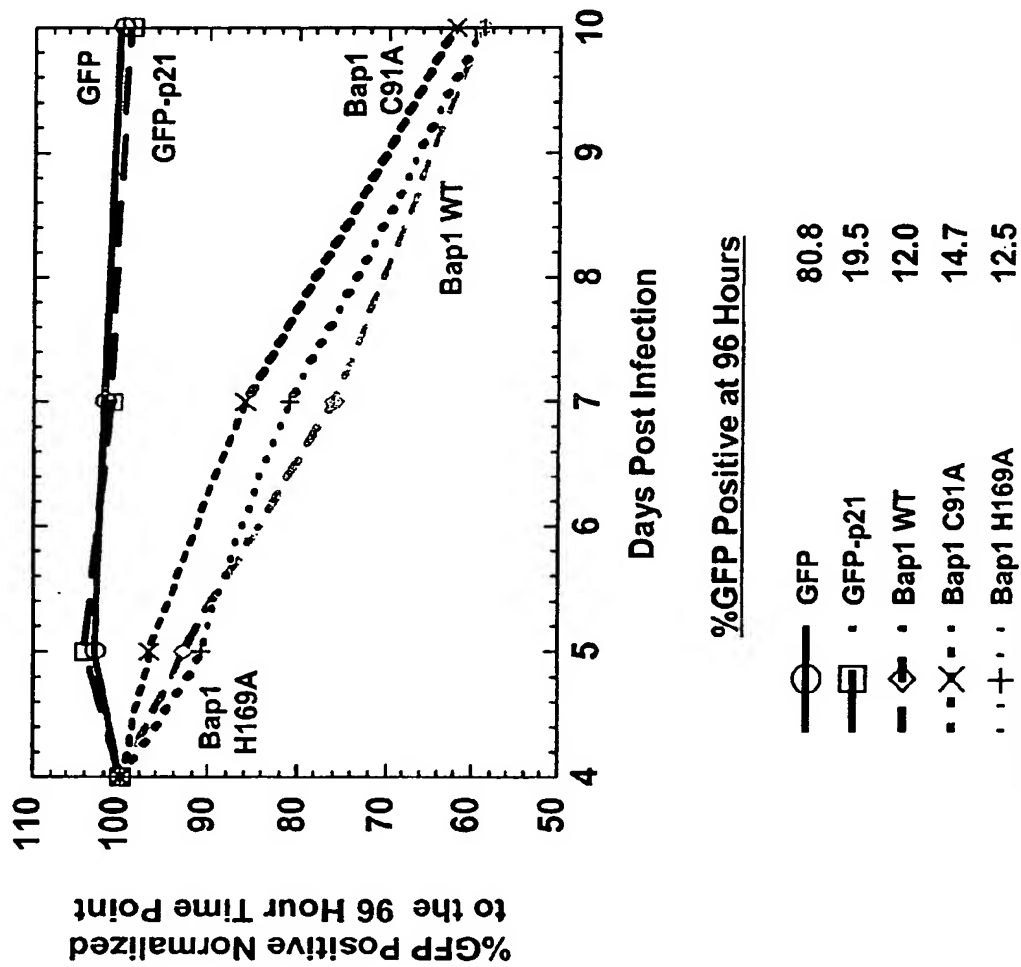


FIG. 30

RI CEL

Expression of Bap1 WT Protein is Antiproliferative in HeLa Cells in the Celltracker Assay

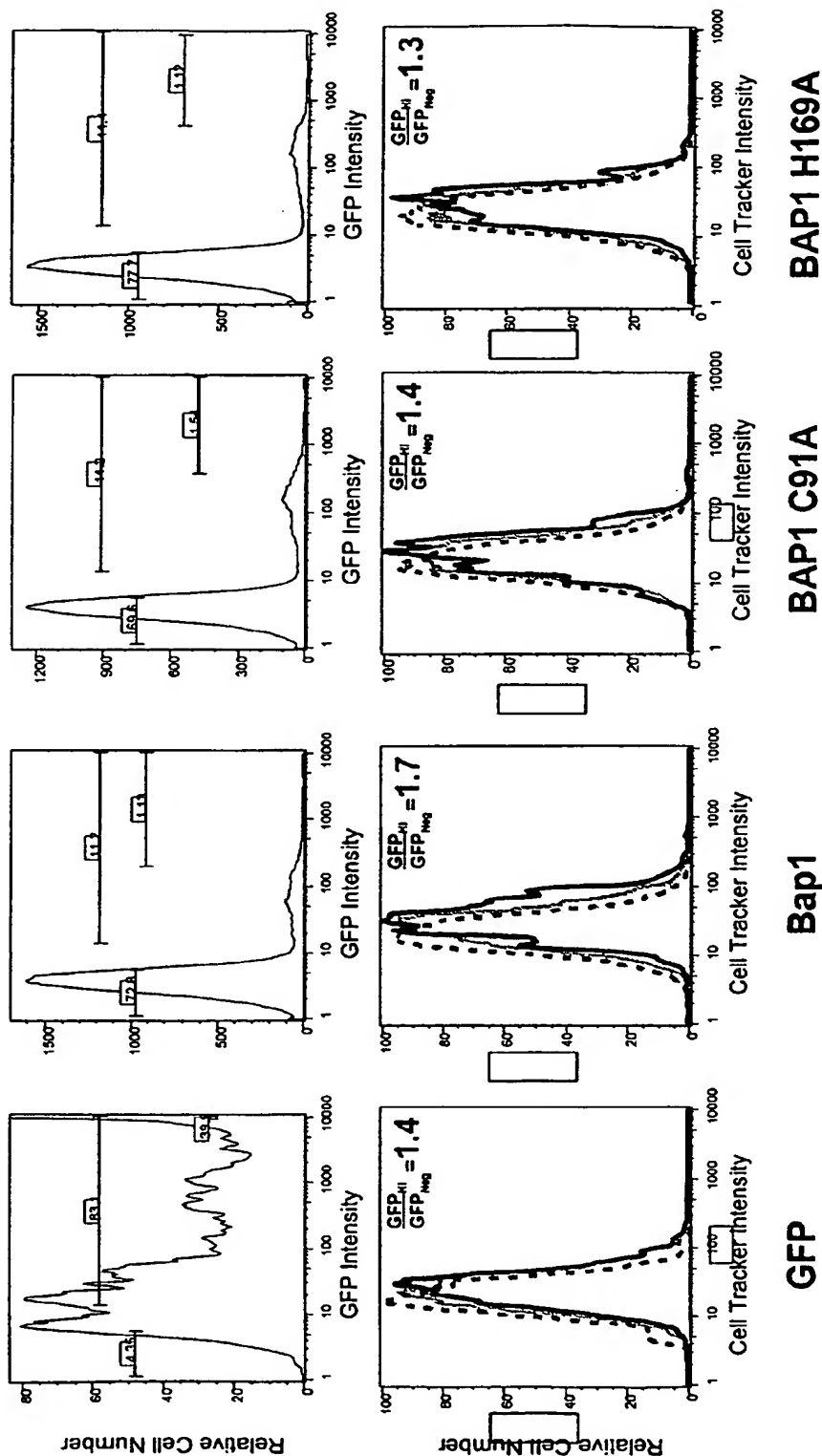


FIG. 31

R I G E L

10/510903

Expression of Bap1 Protease Mutants is Slightly More Antiproliferative Than Expression of Bap1 WT in H1299 Cells

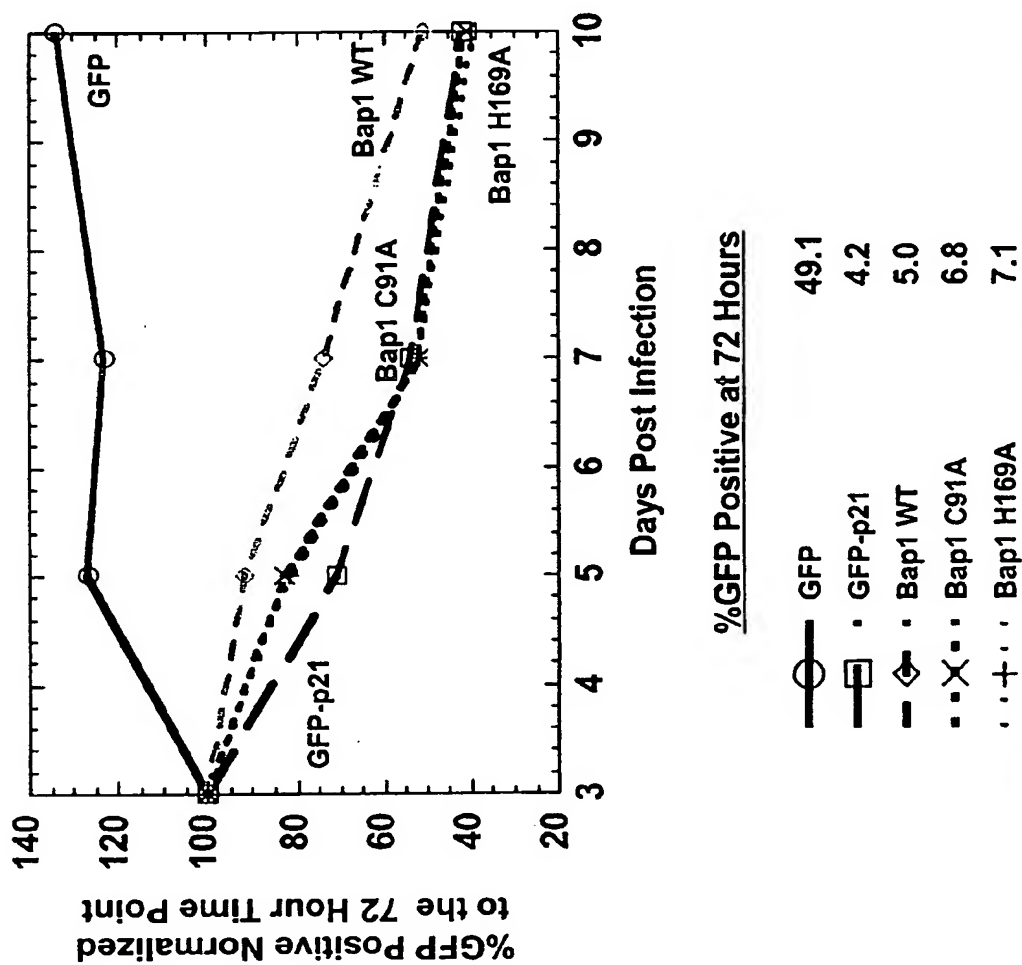
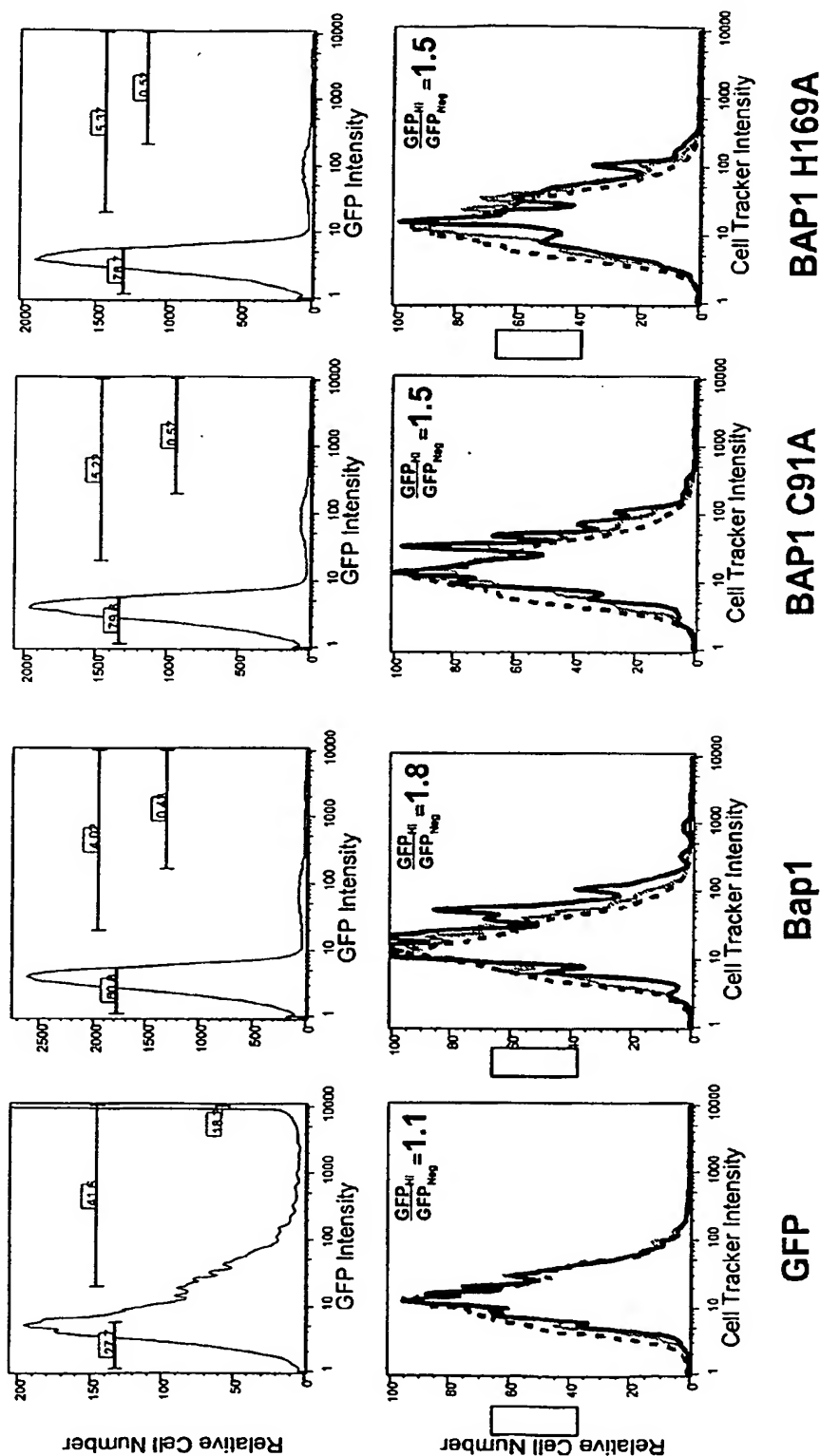


FIG. 32

R 10/510903

Expression of Bap1 WT and Bap1 Protease Mutants is Antiproliferative in H1299 Cells in the Celltracker Assay



Cell Tracker Assay Day 5 GFP+ --- GFP- — GFP Hi

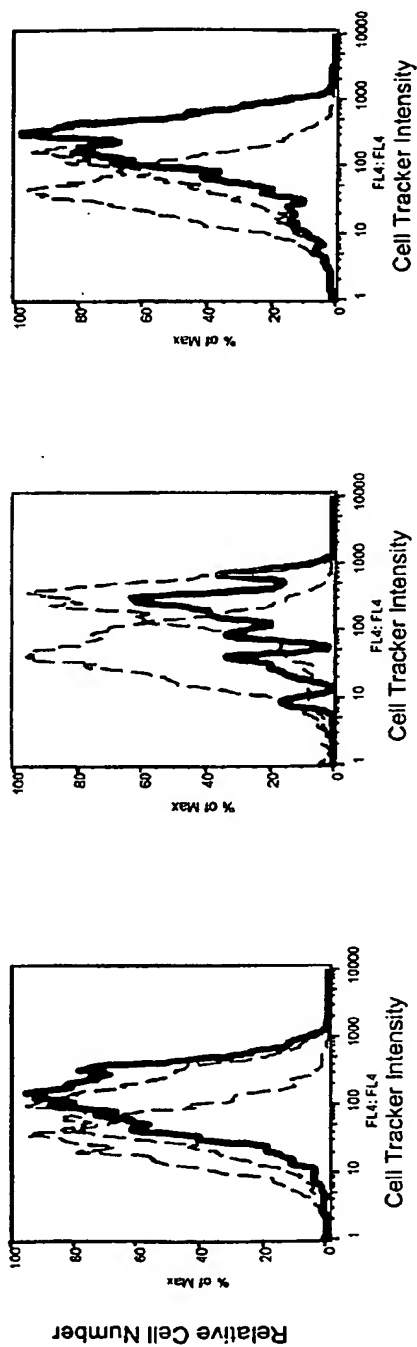
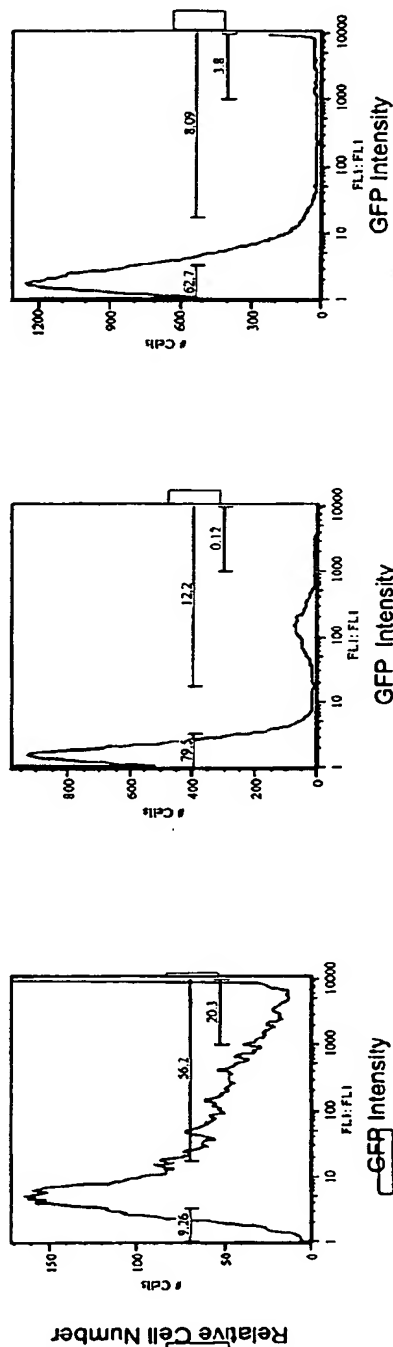
$\frac{GFP_{Hi}}{GFP_{Neg}} = \frac{(\text{mean celltracker intensity of } GFP_{Hi})}{(\text{mean cell tracker intensity of } GFP_{Neg})}$

FIG. 33

R G E L

10/510903

The Bap1 Functional Hit G32D8 is Antiproliferative in HMEC Cells



G32D8

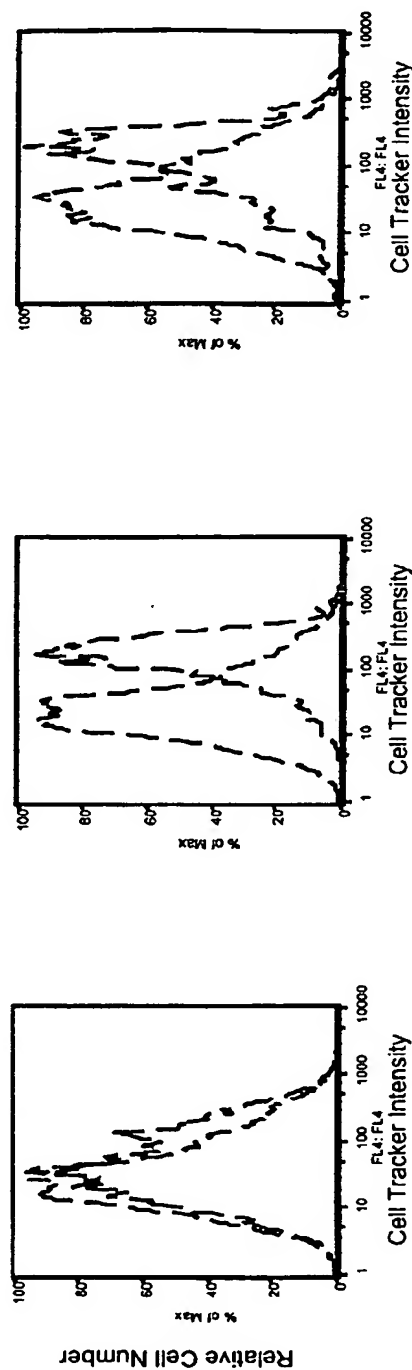
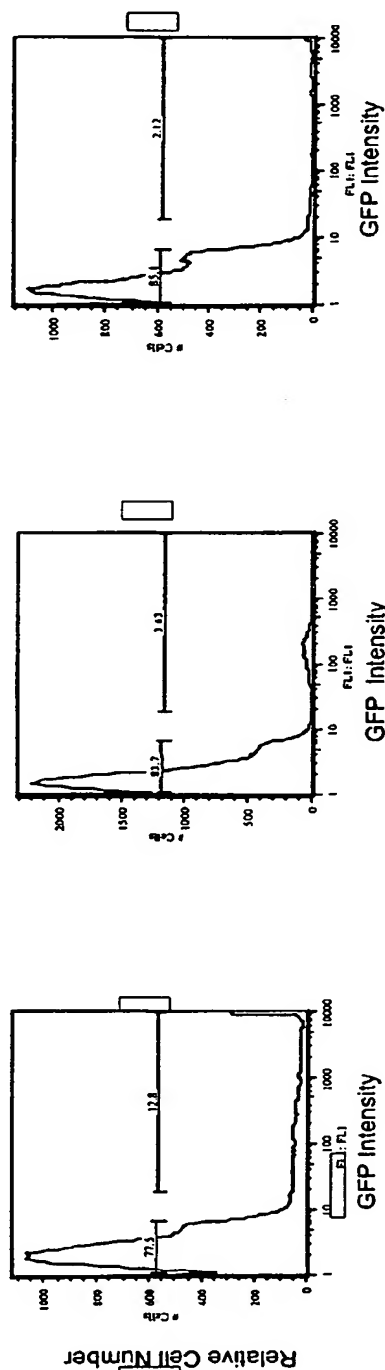
Gp21

GFP

..... GFP+ --- GFP- — GFP hi

FIG. 34

The Bap1 Functional Hit G3-2D8 is Antiproliferative in PrEC Cells



Gp21

G3-2D8

GFP

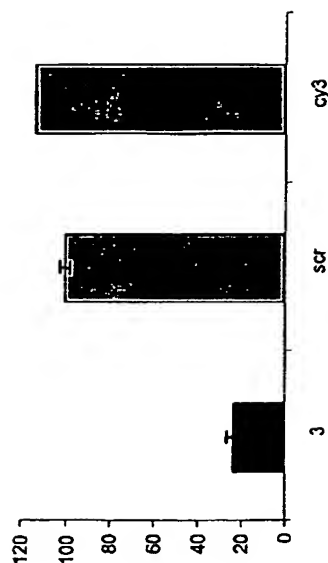
..... GFP+ --- GFP- — GFP hi

FIG. 35

PrEC

BAP1 Specific siRNA Has an Antiproliferative Effect on HeLa Cells

BAP1 mRNA levels in HeLa after siRNA treatment (Taqman)



HeLa cell cycle profile after BAP1 siRNA treatment



BrdU incorporation by HeLa treated with BAP1 siRNA

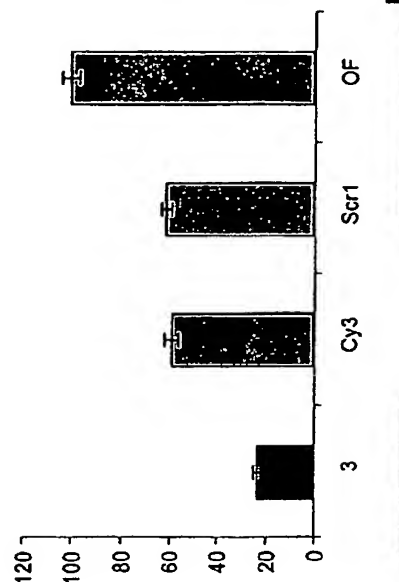


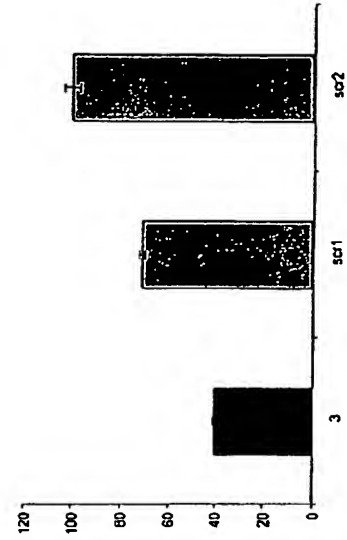
FIG. 36

BAP1 Specific siRNA Induces G1 Arrest in H1299 Cells

BAP1 mRNA levels in H1299 after siRNA treatment (Taqman)



BrdU incorporation by H1299 treated with BAP1 siRNA



H1299 cell cycle profile after BAP1 siRNA treatment

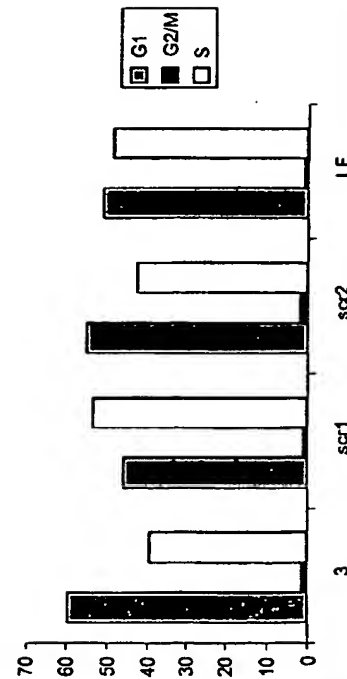
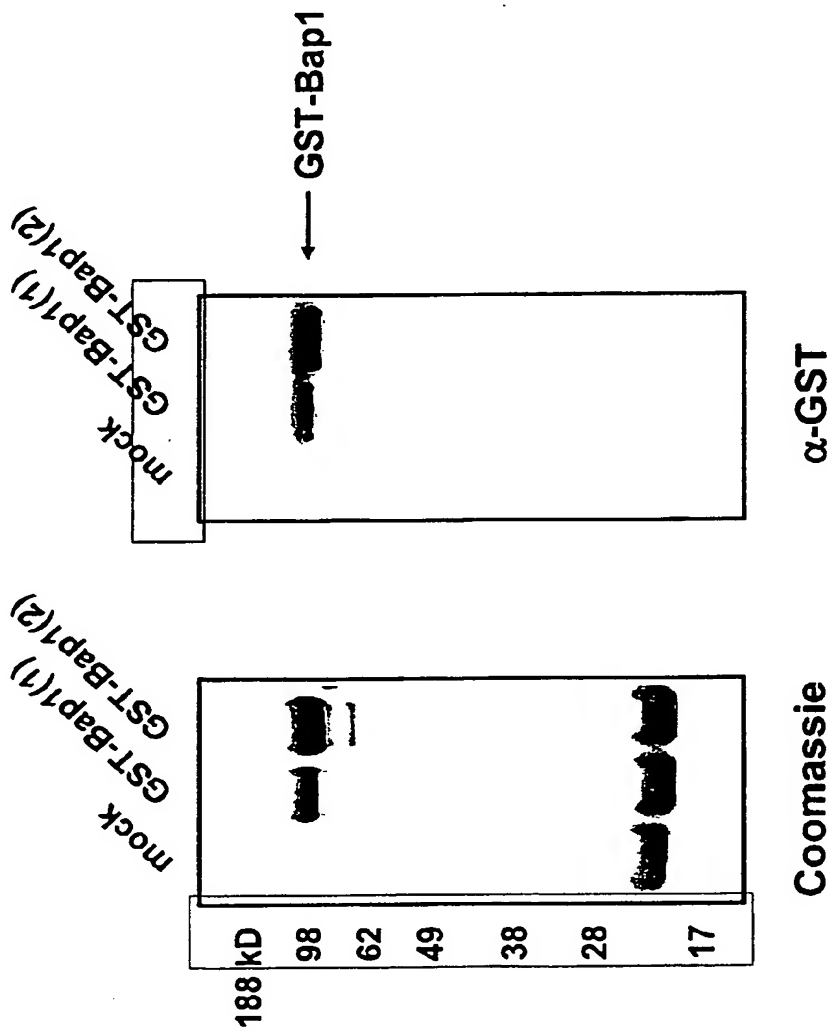


FIG. 37

REL

Soluble GST-Bap1 Protein can be Expressed from SF9 Cells



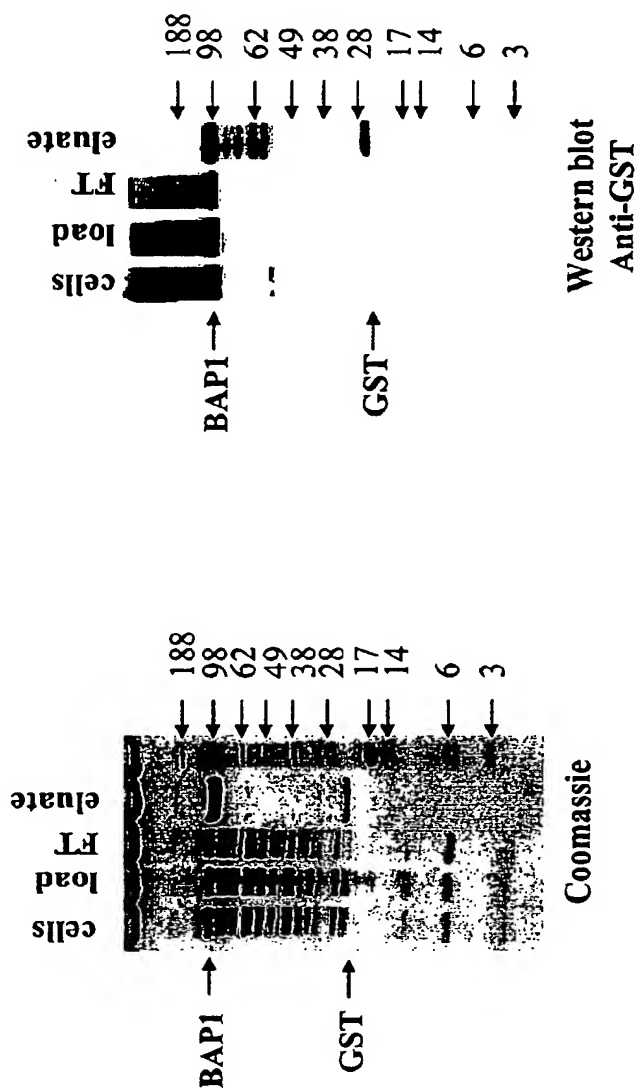
GST-Bap1 was produced using the baculovirus transfer vector pDEST20 along with the Bac-to-Bac baculovirus expression system (Invitrogen). GST-Bap1(1) and GST-Bap1(2) refer to two different virus dilutions used for expression.

FIG. 38

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BAP1 purification



RIGEL

FIG. 39

Example of Fluorogenic Ub Cleavage Assay

Aminomethyl-coumarin cleavage from Ub C-terminus
generates fluorescence emission in solution-phase assay

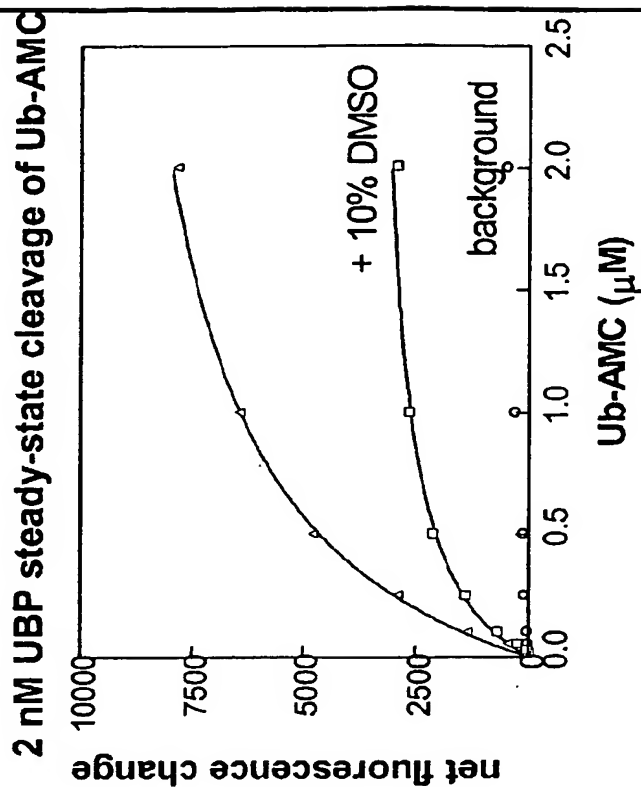
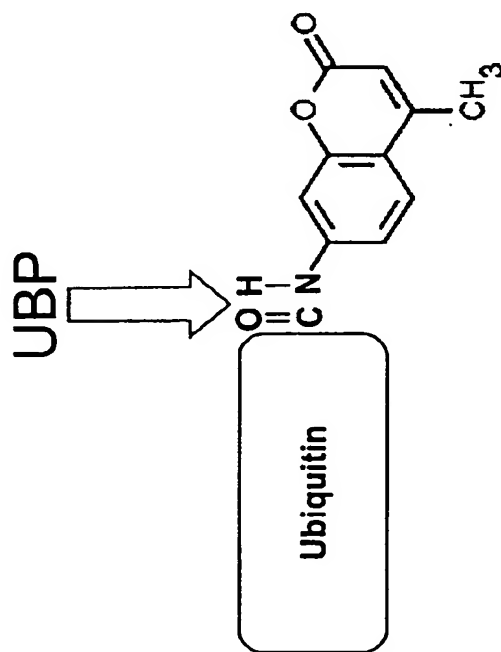


FIG. 40

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BAP1 is an Active Ubiquitin Protease

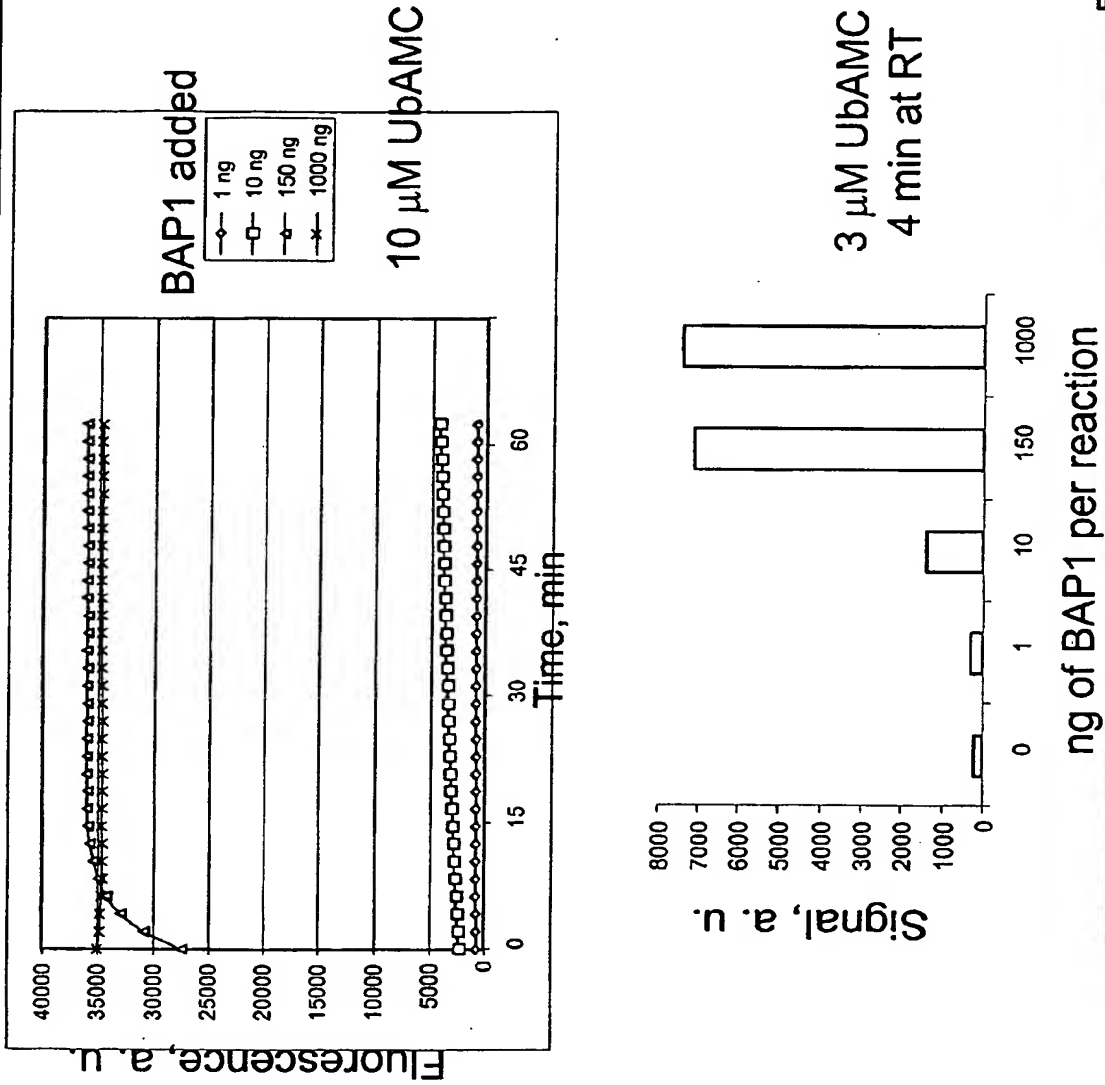
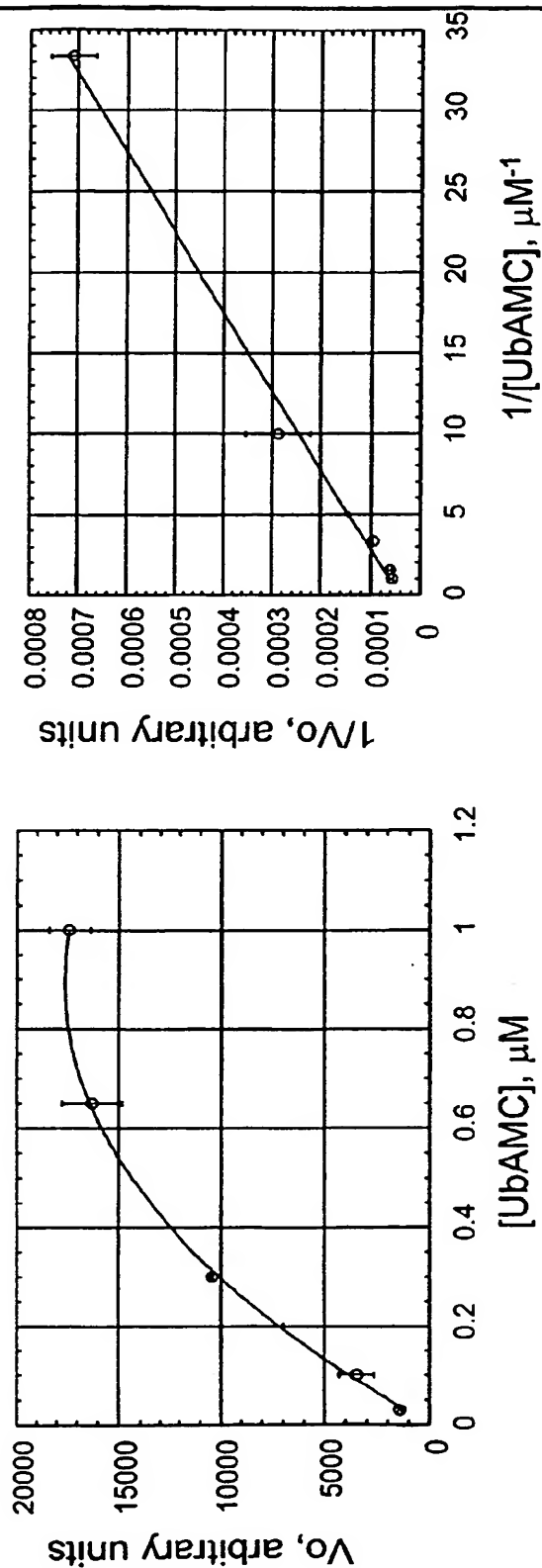


FIG. 41

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Kinetics of UbAMC cleavage by BAP1

 $K_m = 0.5 \mu M$

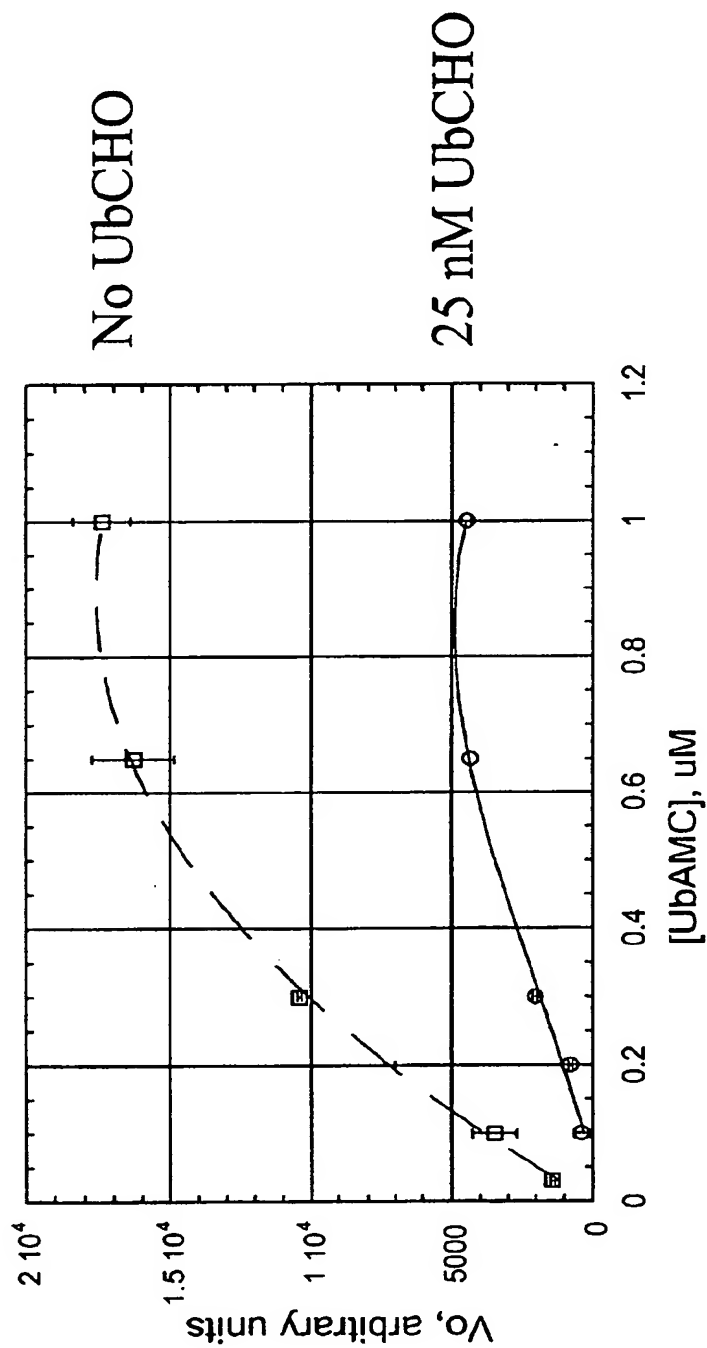
1 ng of BAP1 per well
(0.1 nM BAP1)

FIG. 42

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UbCHO Acts as Specific Inhibitor of BAP1

 $K_i = 9 \text{ nM}$

1 ng of BAP1 per well
(0.1 nM BAP1)

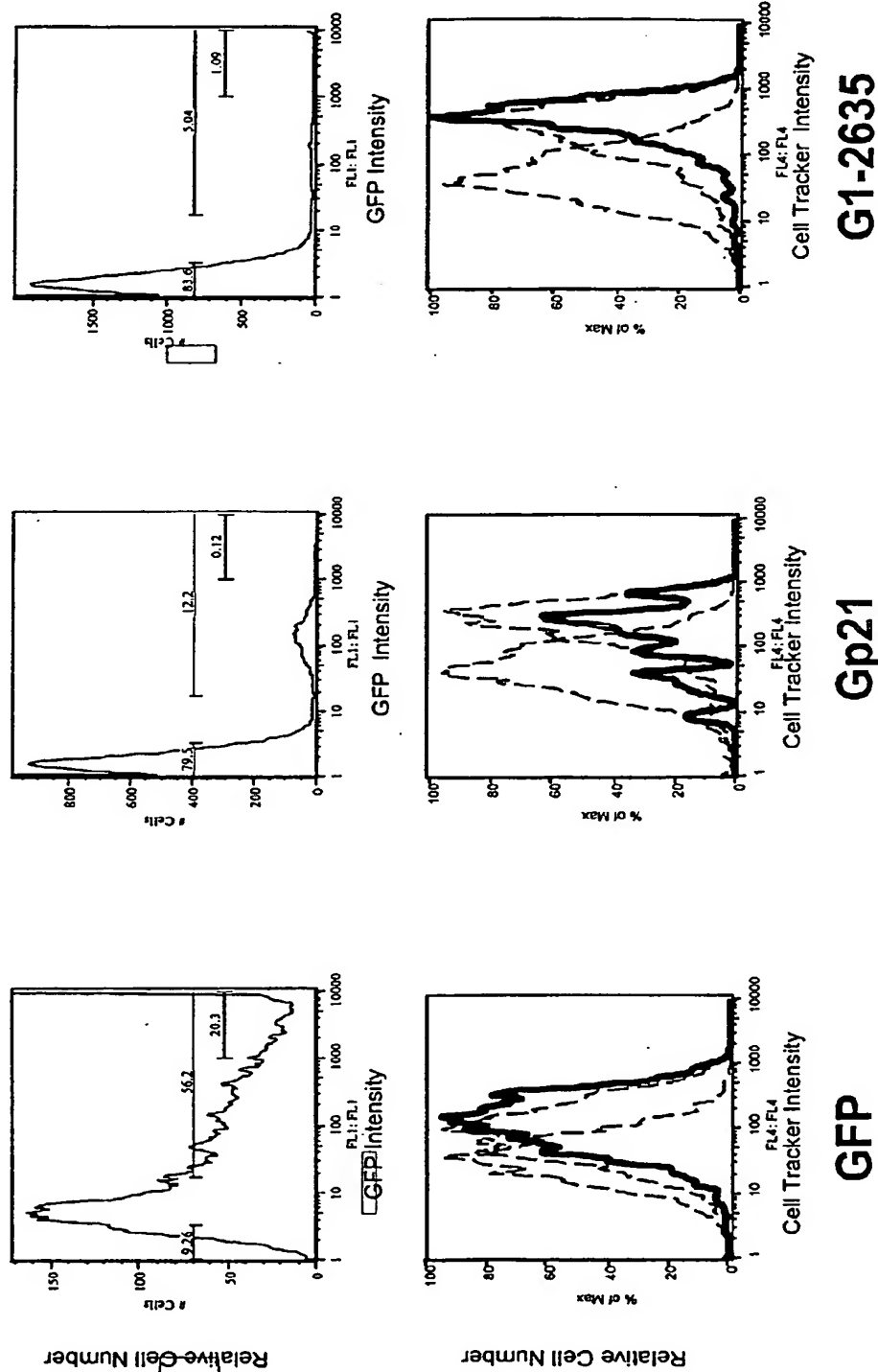
FIG. 43

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Cell Line: HMEC

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The Np95 Functional Hit G1-2635 is Antiproliferative in HMEC Cells



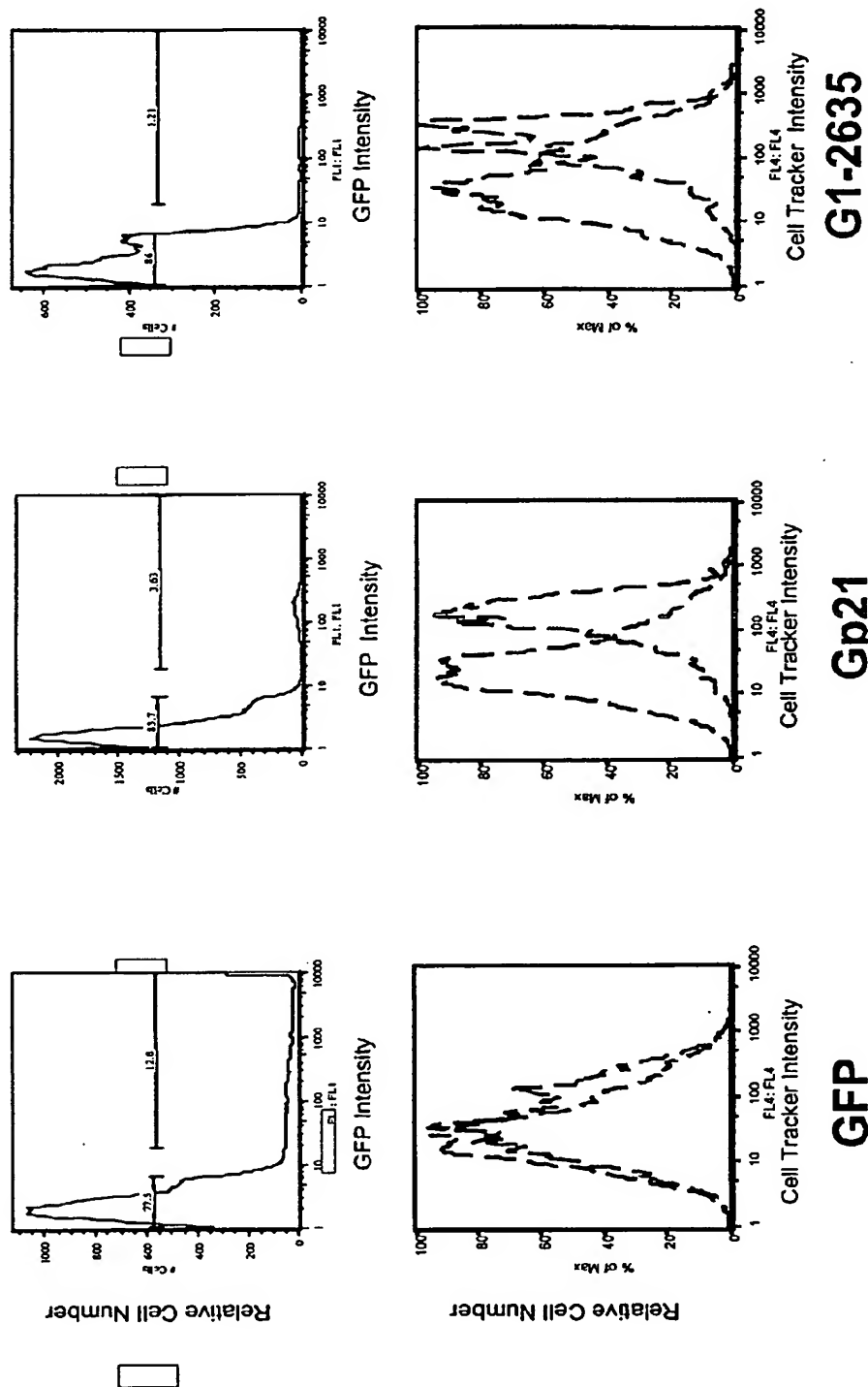
..... GFP+ --- GFP- — GFP Hi

FIG. 44

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The Np95 Functional Hit G1-2635 is Antiproliferative in PrEC Cells



..... GFP+ ---- GFP-

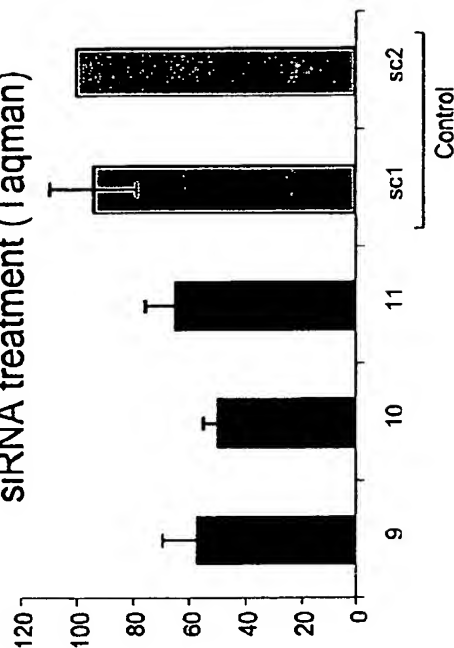
FIG. 45

RIJGEL

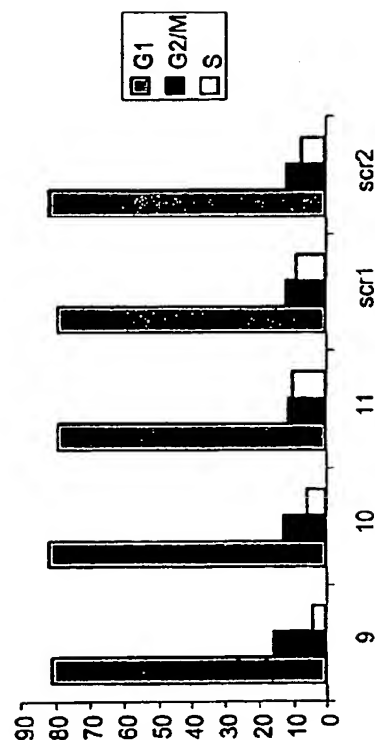
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NP95 Specific siRNAs Have Antiproliferative Effect on PrECs

NP95 mRNA levels in PrEC after siRNA treatment (Taqman)



PrEC cell cycle profile after NP95 siRNA treatment



BrdU incorporation by PrEC treated with NP95 siRNAs

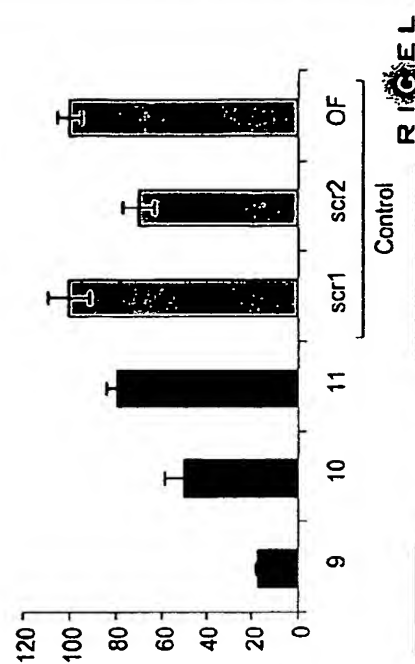
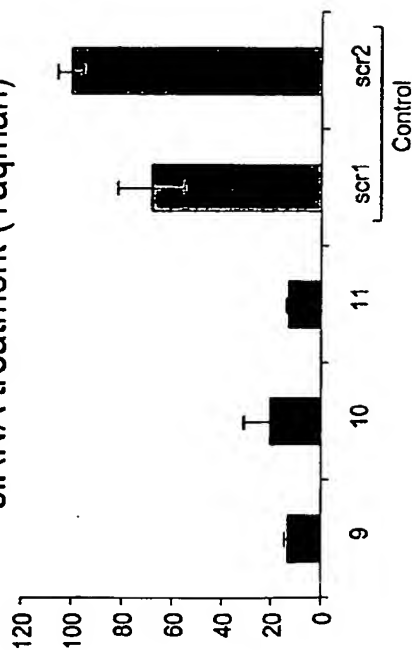


FIG. 46

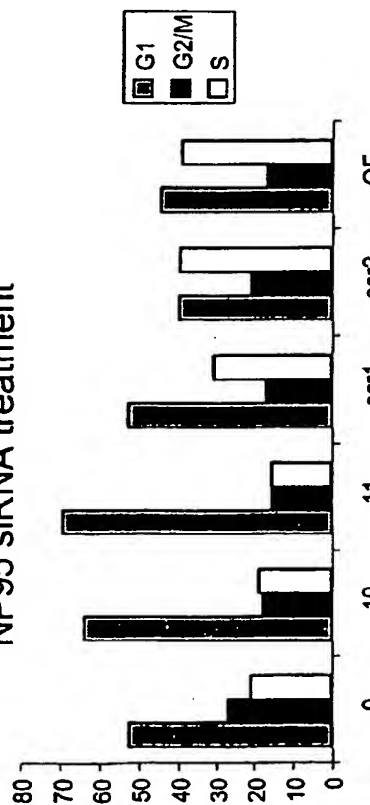
10/510903

NP95 Specific siRNAs Induce G1 Arrest in HUVEC Cells

NP95 mRNA levels in HUVEC after siRNA treatment (Taqman)



HUVEC cell cycle profile after NP95 siRNA treatment



BrdU incorporation by HUVEC treated with NP95 siRNAs

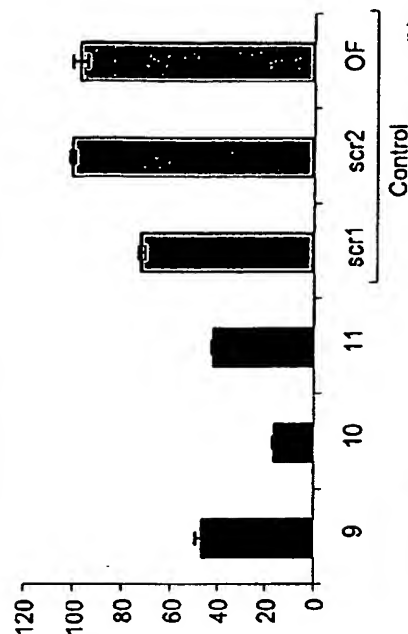
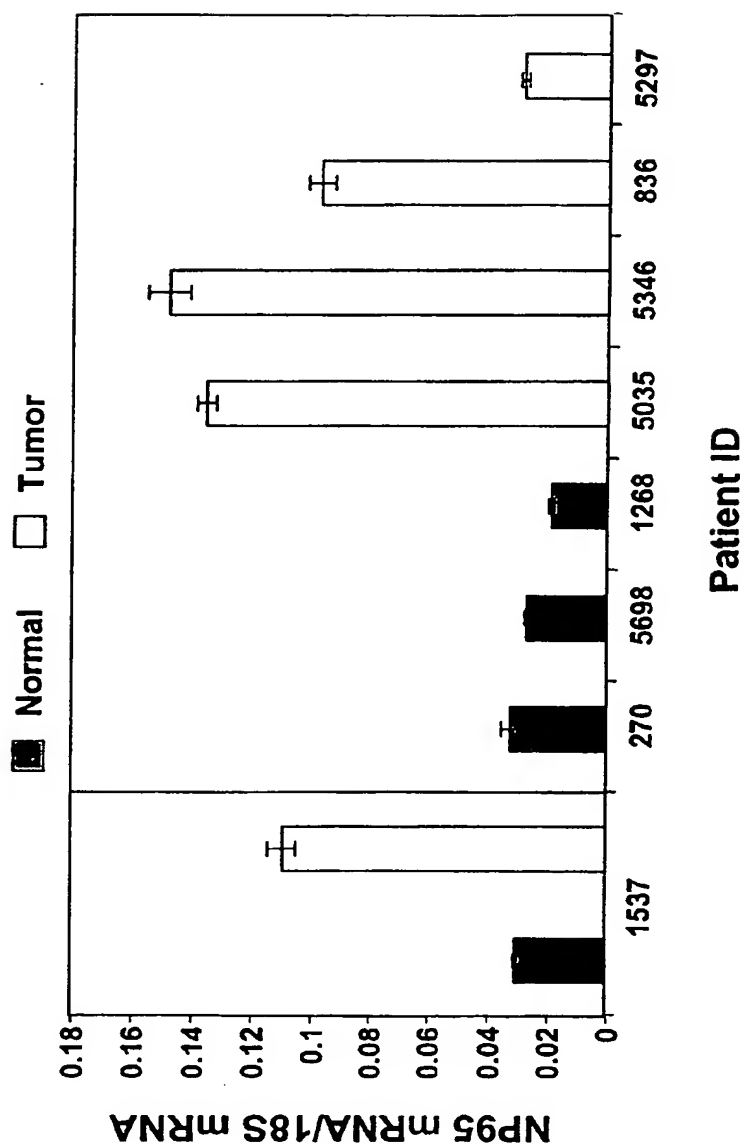


FIG. 47

10/510903

Taqman Analysis of NP95 mRNA Expression in Samples Obtained from Patients with Breast Carcinoma



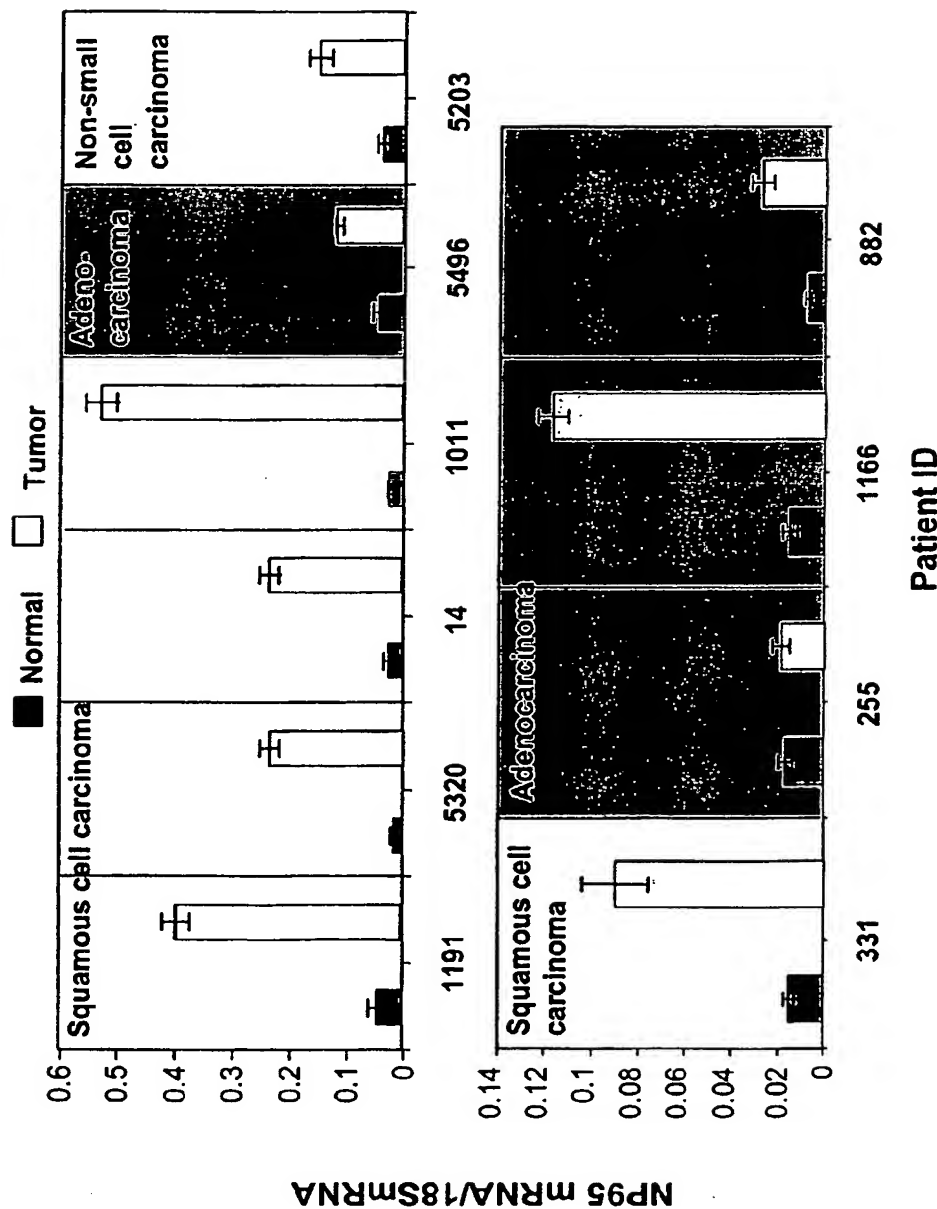
Ductal Adenocarcinoma 836, 1537, 5035, 5346
Lobular Adenocarcinoma 5297

N = 3, 20 ng total RNA/sample

FIG. 48

RIGEL

Quantitative Analysis of NP95 mRNA Expression in Samples Obtained from Patients with Lung Carcinoma



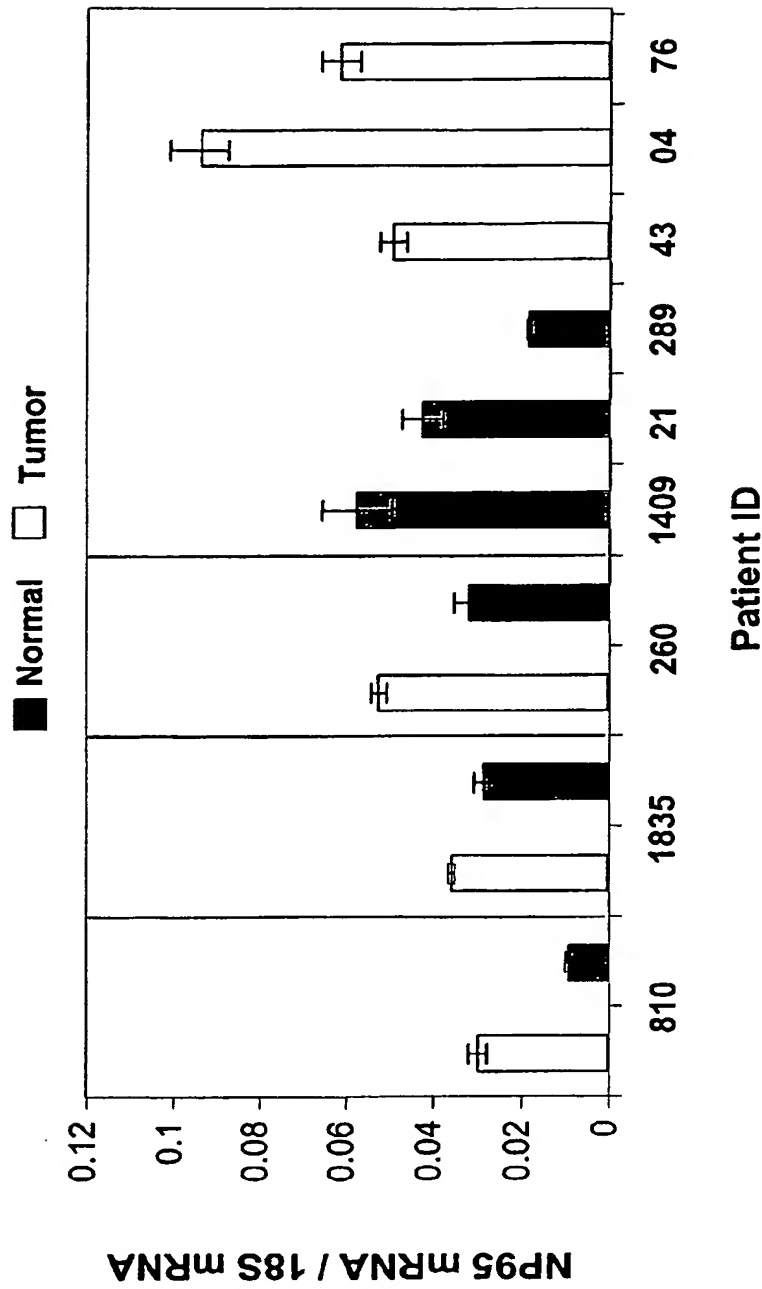
N = 3, 20 ng total RNA/sample

FIG. 49

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Quantitative Analysis of NP95 mRNA Expression in Samples Obtained from Patients with Prostate Adenocarcinoma



All tumors of acinar cell origin
N=3, 20 ng total RNA Sample

FIG. 50

RI CEL

Dominant Negative Mutants of Np95

Np95	WT	UBQ	PHD	G9a	RING
	Δ RING	UBQ	PHD	G9a	
	C724A	UBQ	PHD	G9a	RING
	H741A	UBQ	PHD	G9a	RING

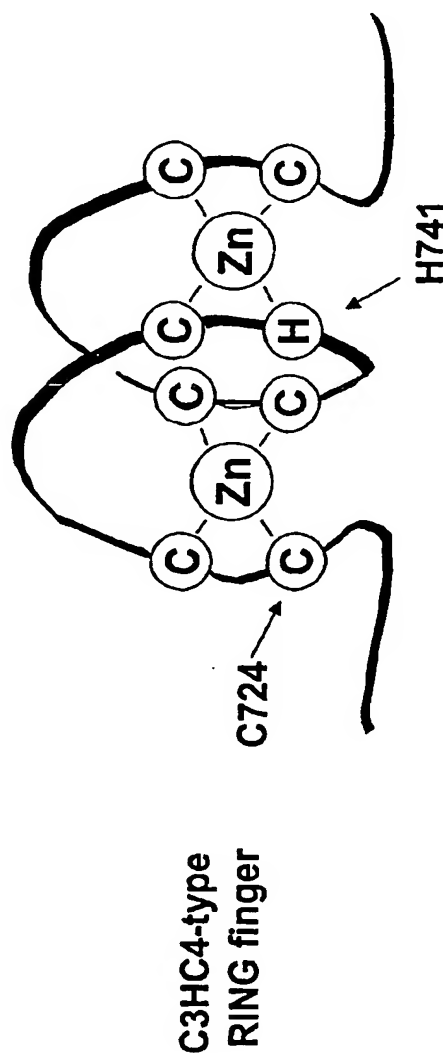
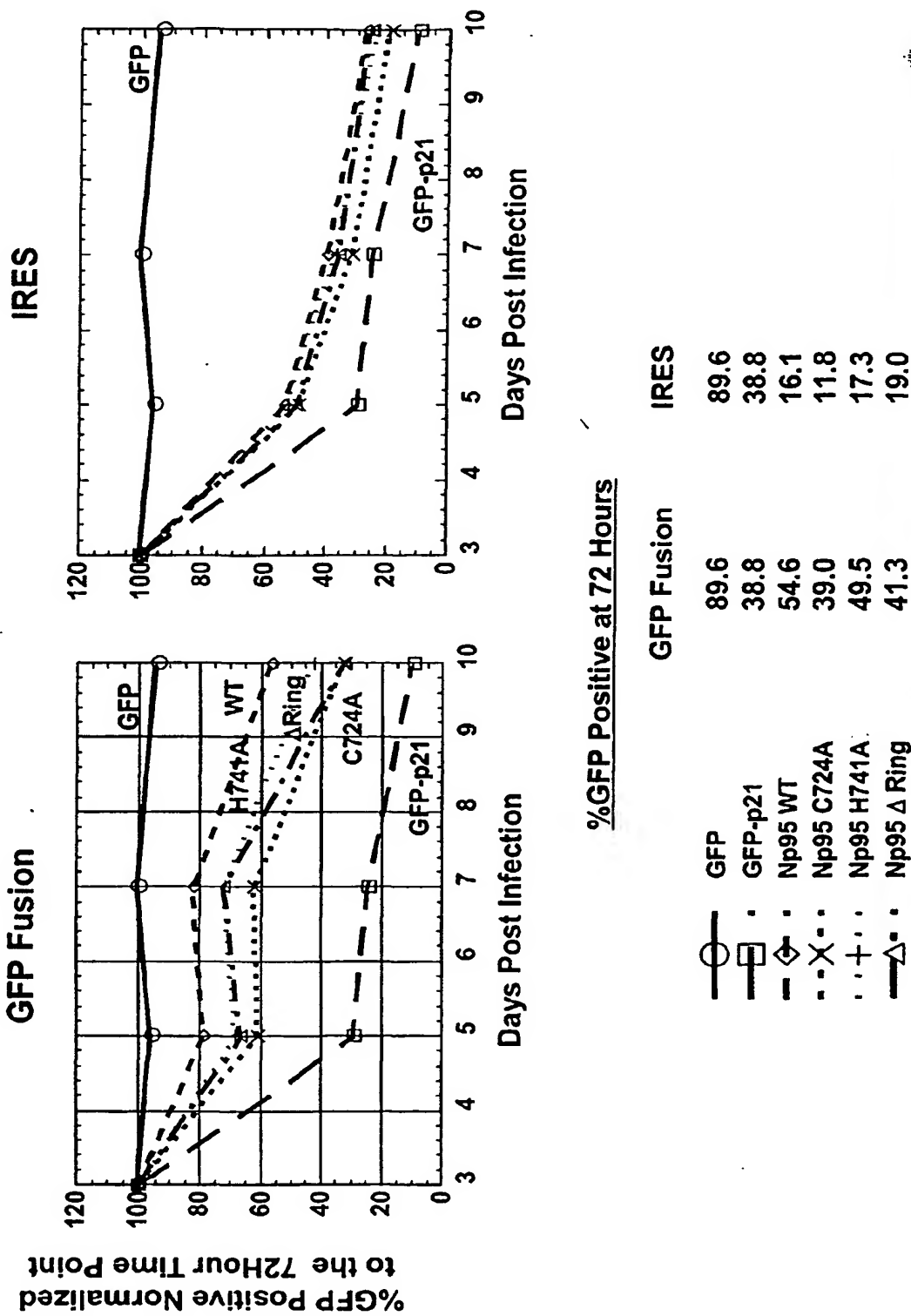


FIG. 51

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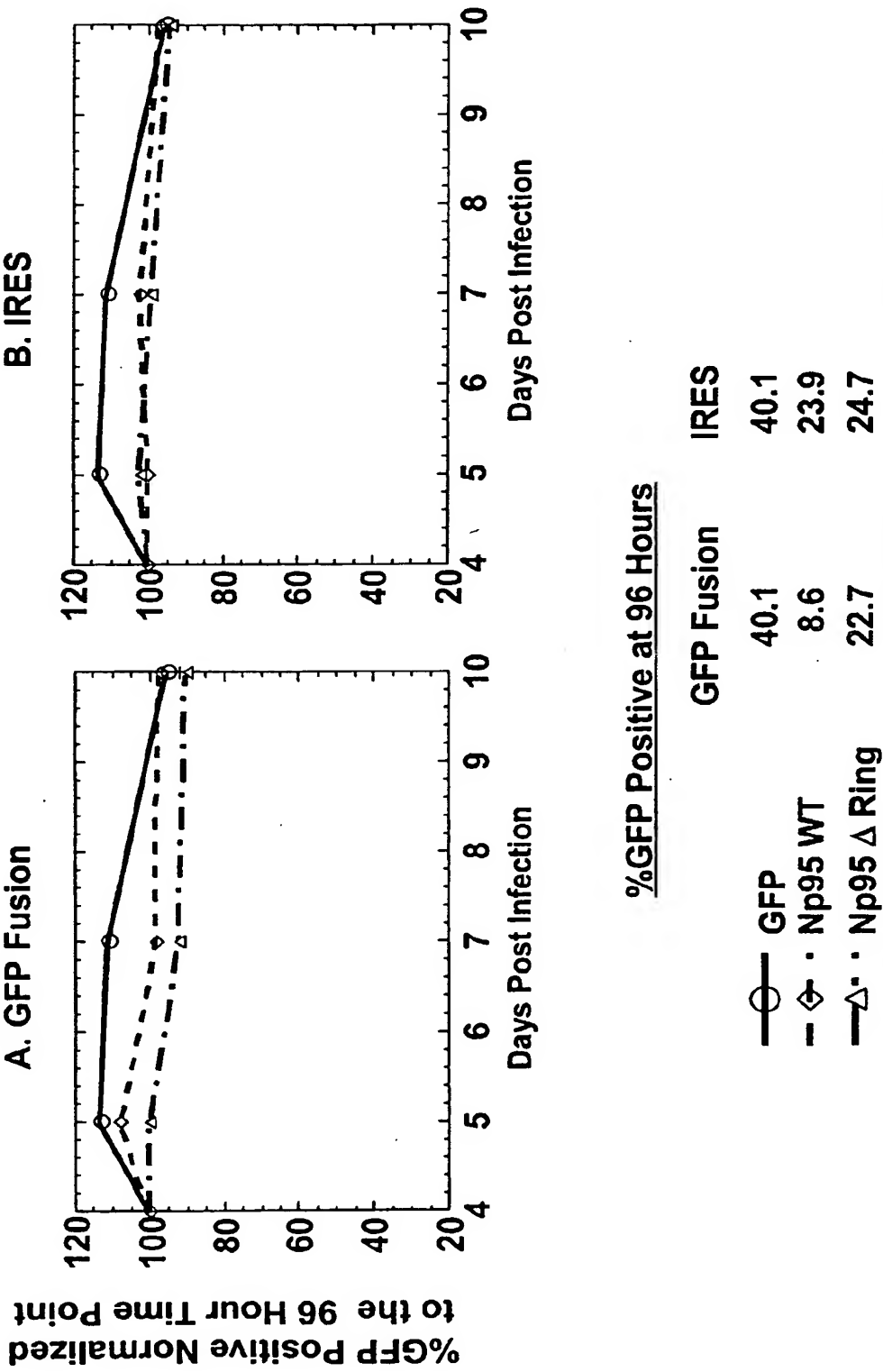
GFP-fused Np95 Ring Finger Mutants are Slightly more Antiproliferative than GFP-fused Np95 WT in HCT116 Cells



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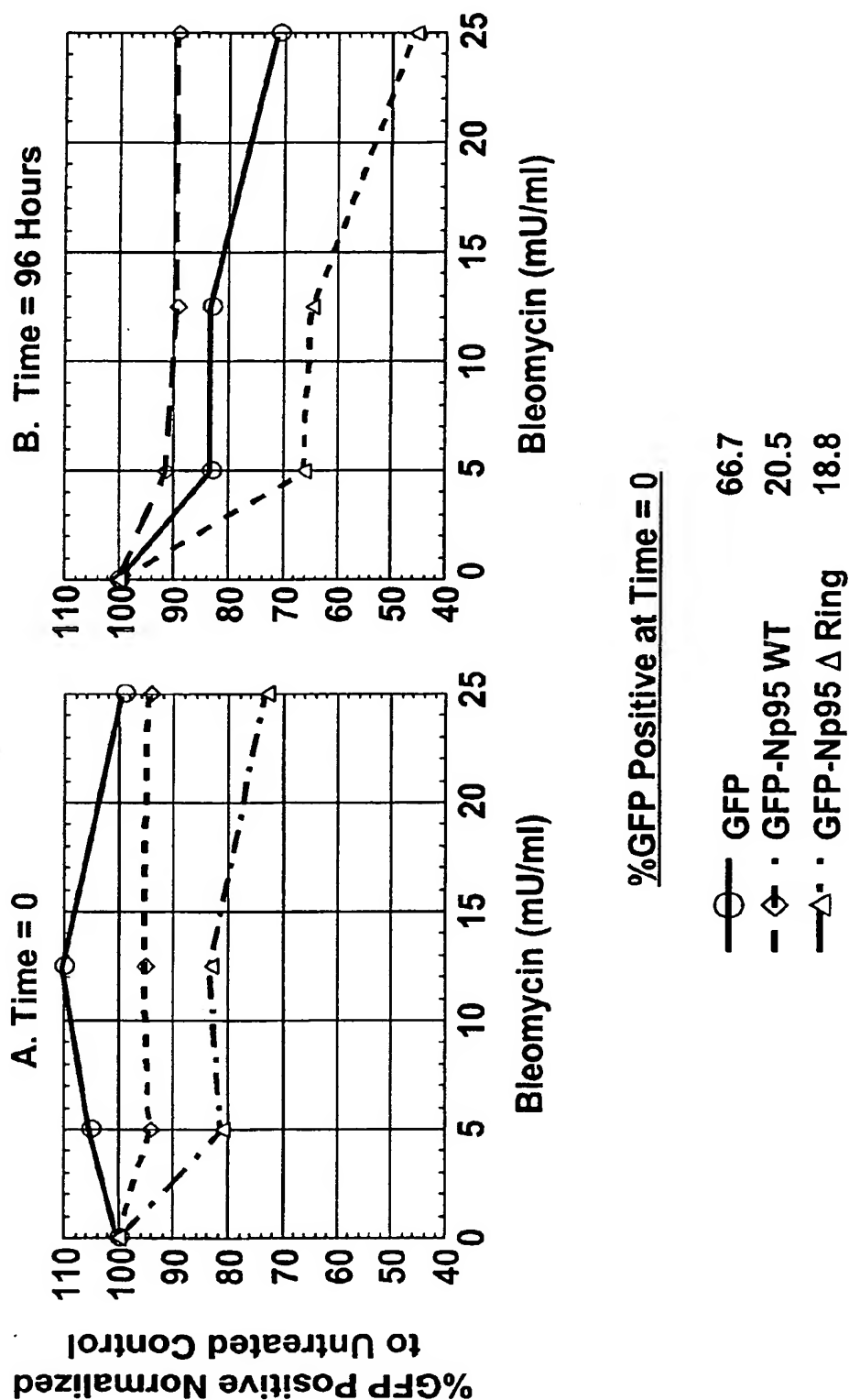
No Antiproliferative Effects Are Observed for Np95 WT and Ring Finger Mutant Constructs in A549 Cells



RIGEL

FIG. 53

A549 Cells Expressing GFP-Np95 Δ Ring Become Sensitized to Bleomycin Treatment



RIGEL

FIG. 54

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Np95 WT and RING Finger Mutant Constructs are Strongly Antiproliferative in HMECs

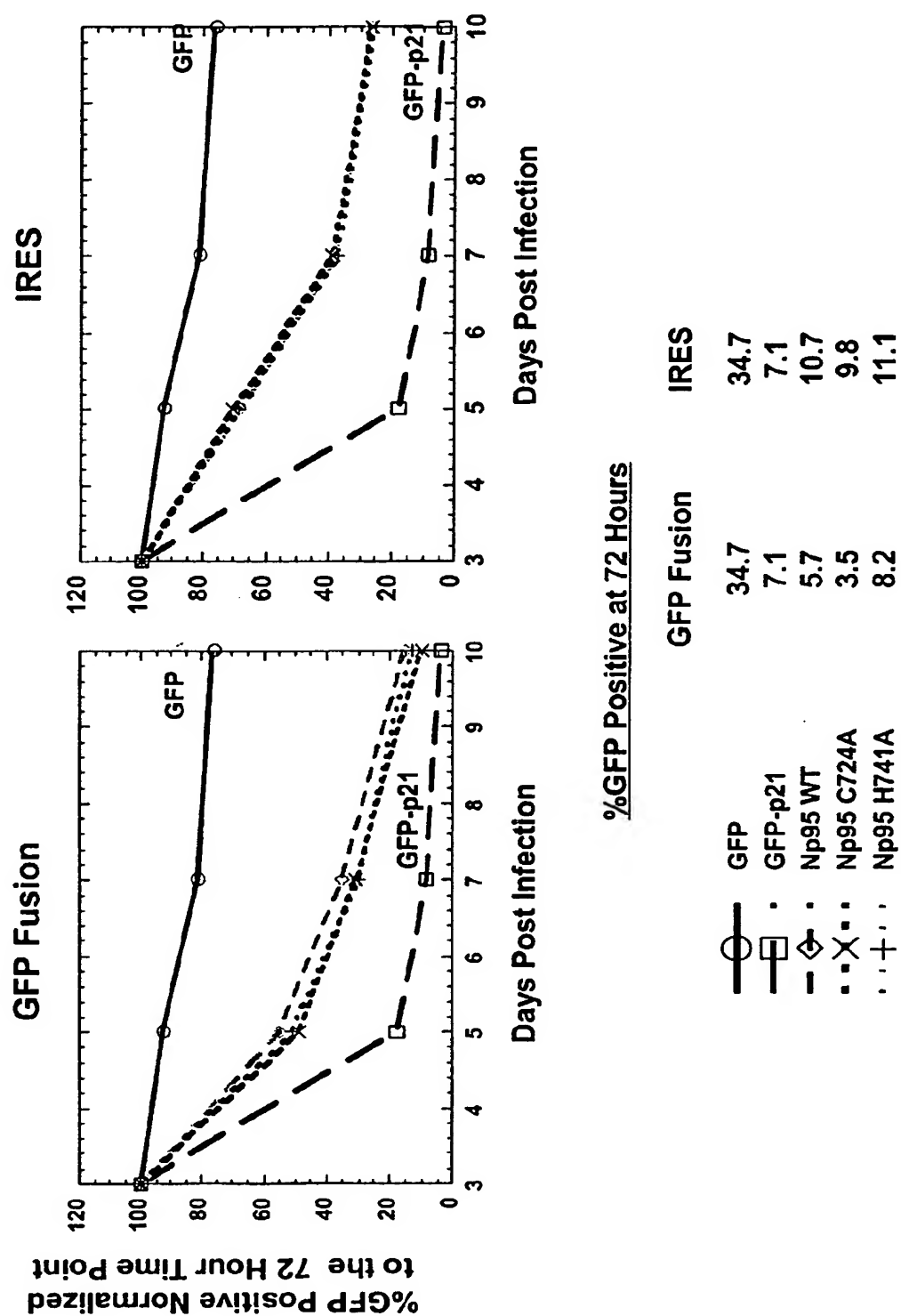
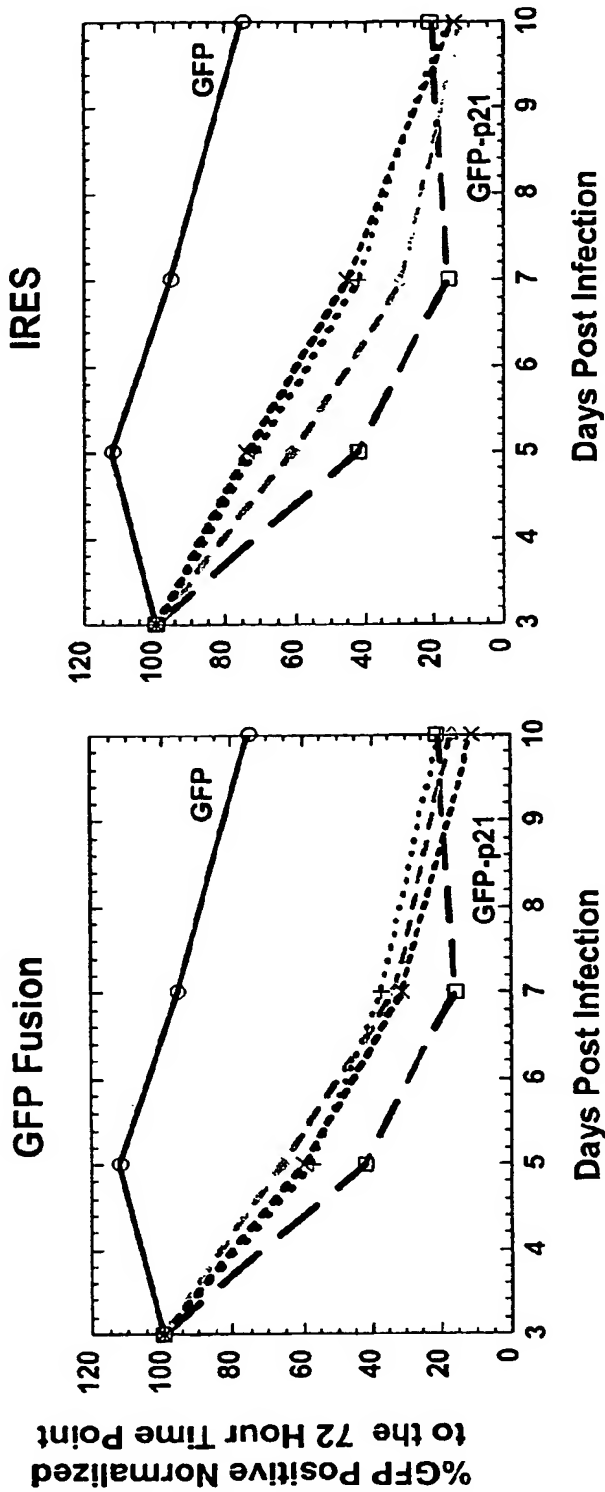


FIG. 55 RIGEL

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Np95 WT and RING Finger Mutant Constructs are Strongly Antiproliferative in PrECs



%GFP Positive at 72 Hours

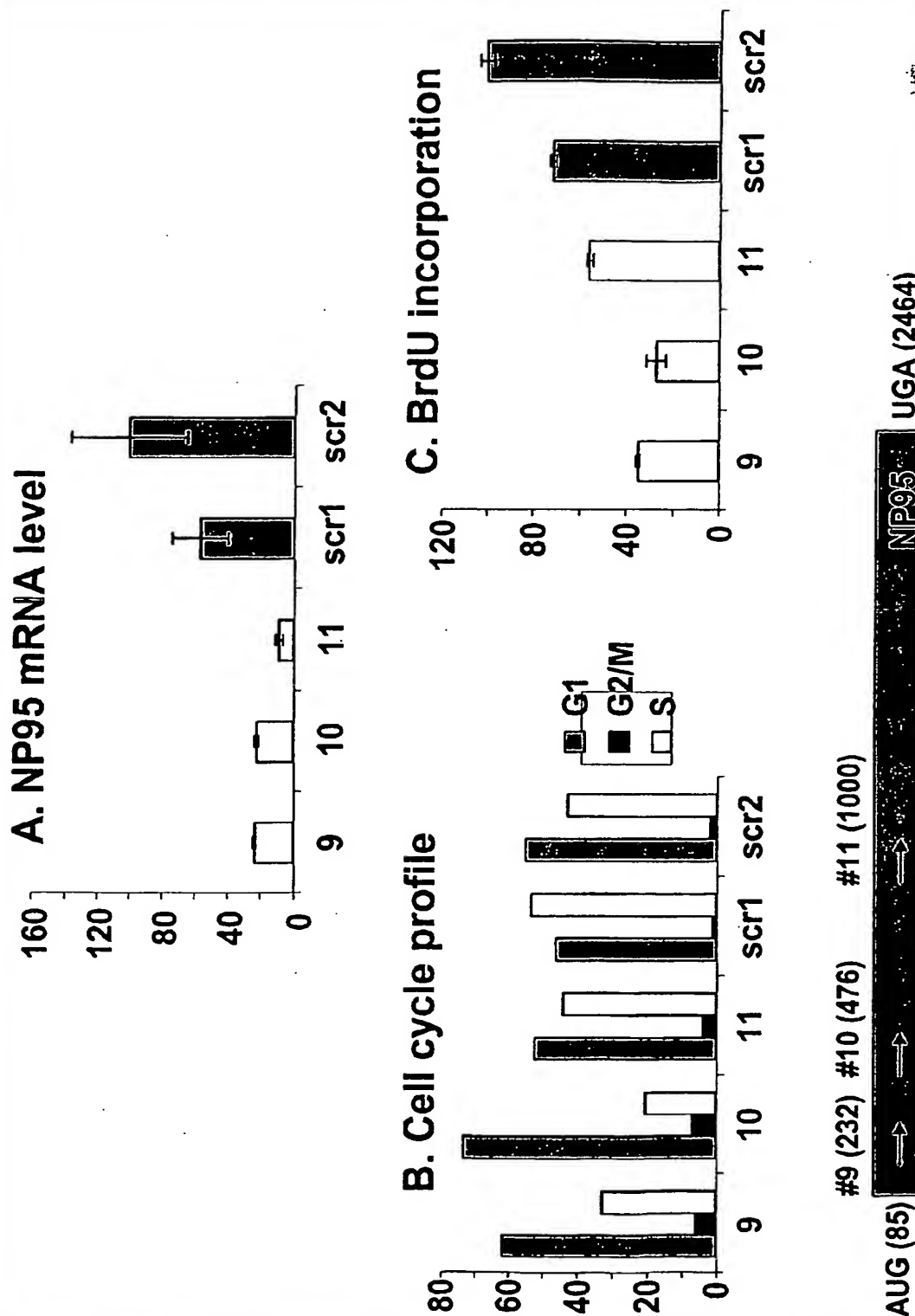
	GFP Fusion	IRES
GFP	10.6	10.6
GFP-p21	1.6	1.6
Np95 WT	1.7	2.7
Np95 C724A	0.91	2.3
Np95 H741A	2.2	2.4

FIG. 56

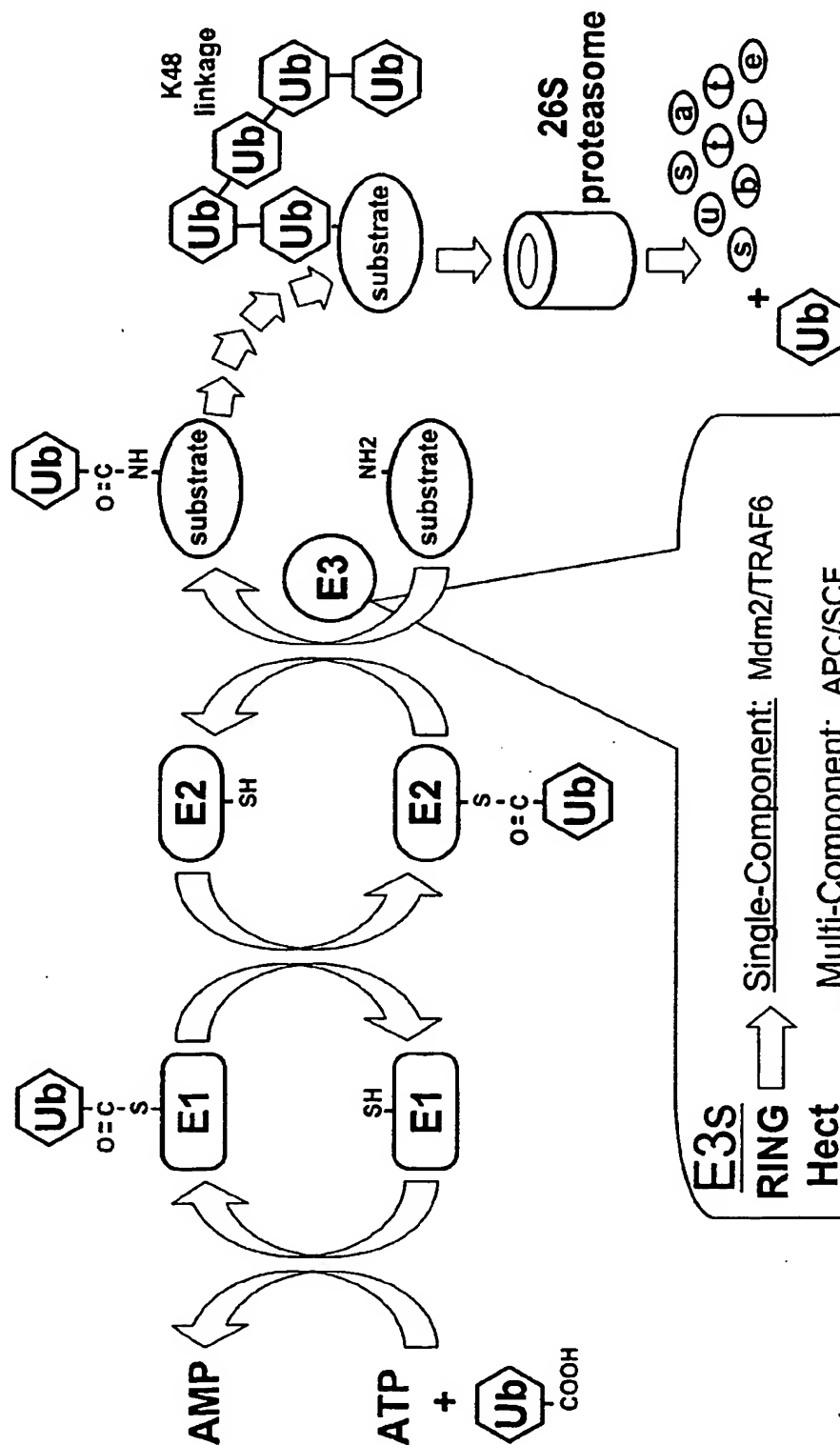
RING

10/510903

NP95-specific siRNAs are Antiproliferative in H1299 Cells



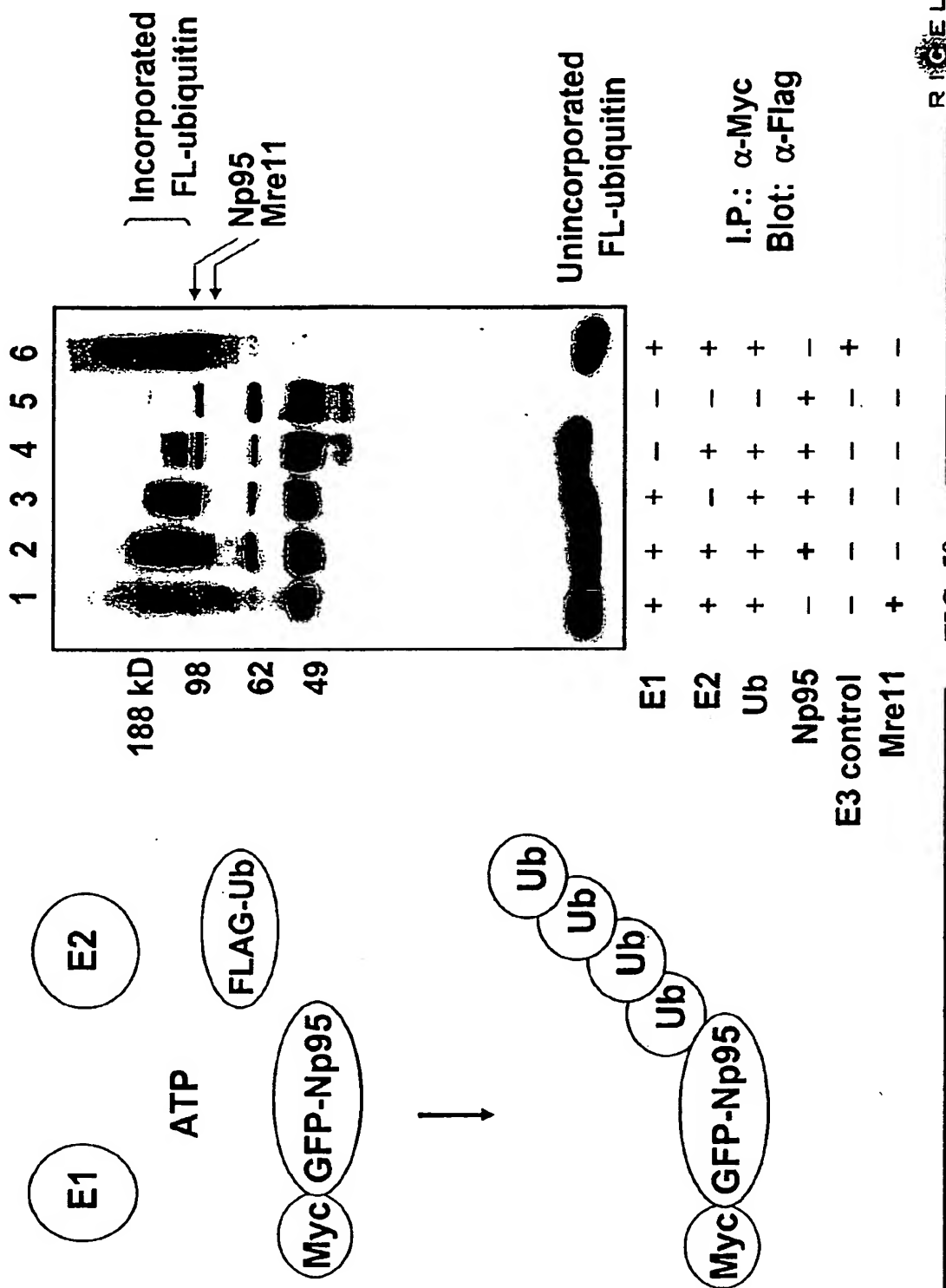
The Biochemistry of Ubiquitylation



RIGEL

FIG. 58

GFP-Np95 Exhibits E3 Ubiquitin Ligase Activity



The RING Domain is Required for GFP-Np95 Ligase Activity

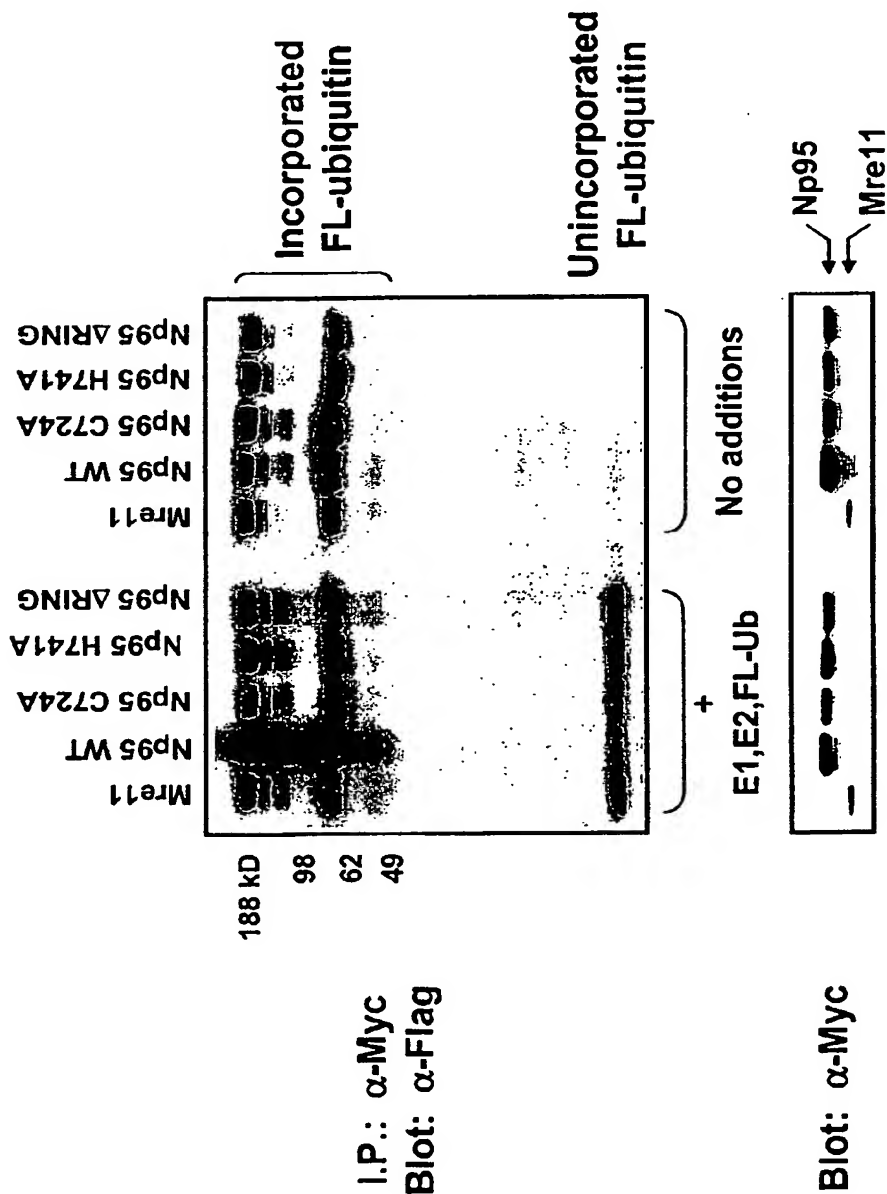
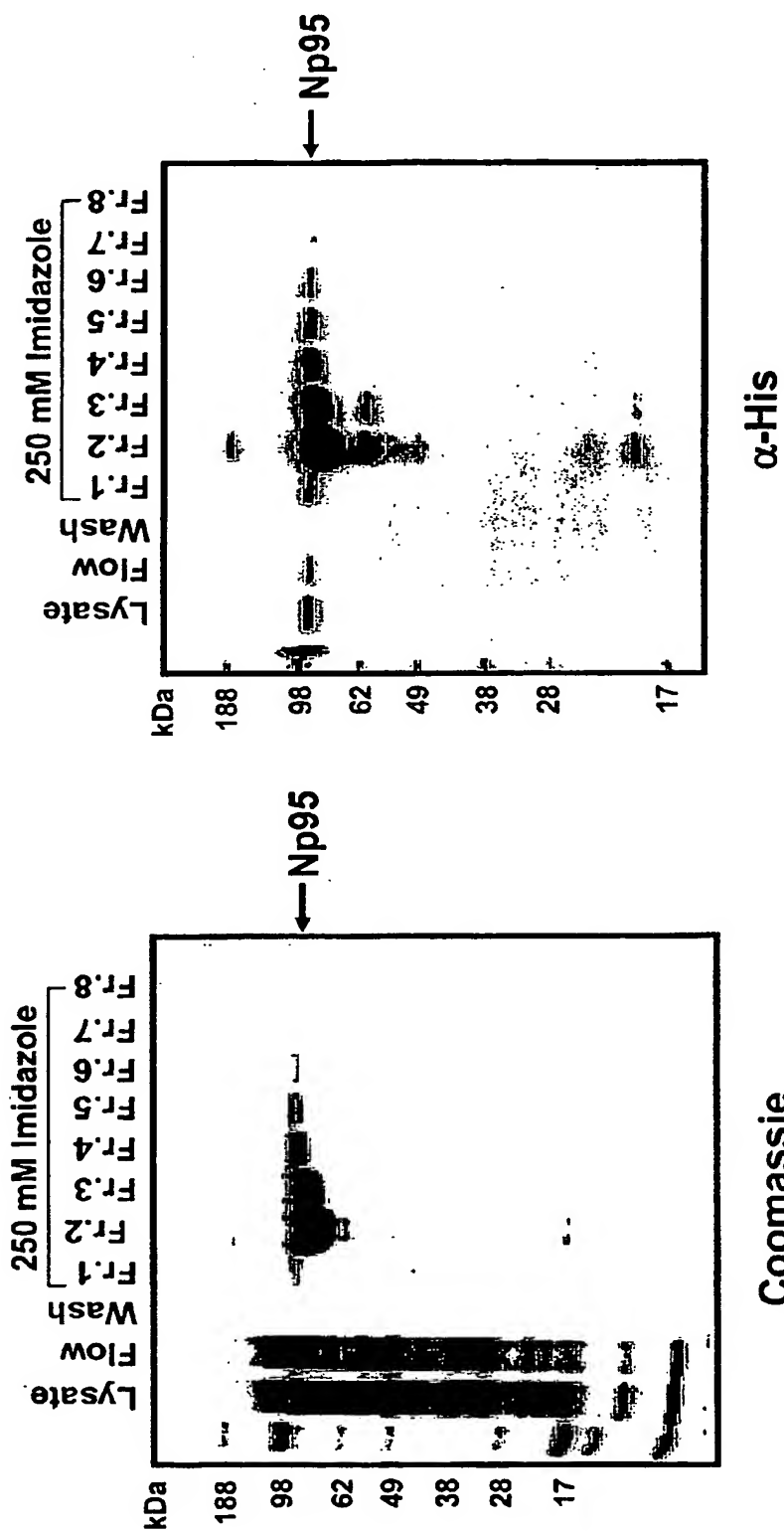


FIG. 60

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Np95 WT Can be Expressed and Purified from SF9 Cells



Yield: ~2.5 mgs/400 million cells

FIG. 61

RIEDEL

10/510903

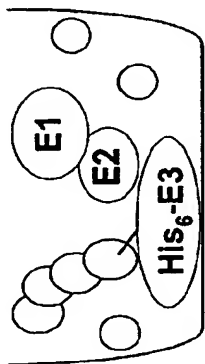
Rigel Plate-Based Ubiquitin Ligase Assay

Nickel coated Plate

○ Flag-Ubiquitin

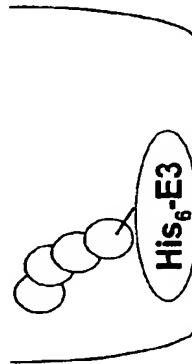
Ligase assay reaction
buffer containing Flag-Ubiquitin

↓ Add E1, E2, and His₆-E3



1 Hr. at room temp.

↓ Wash unbound Flag-Ubiquitin



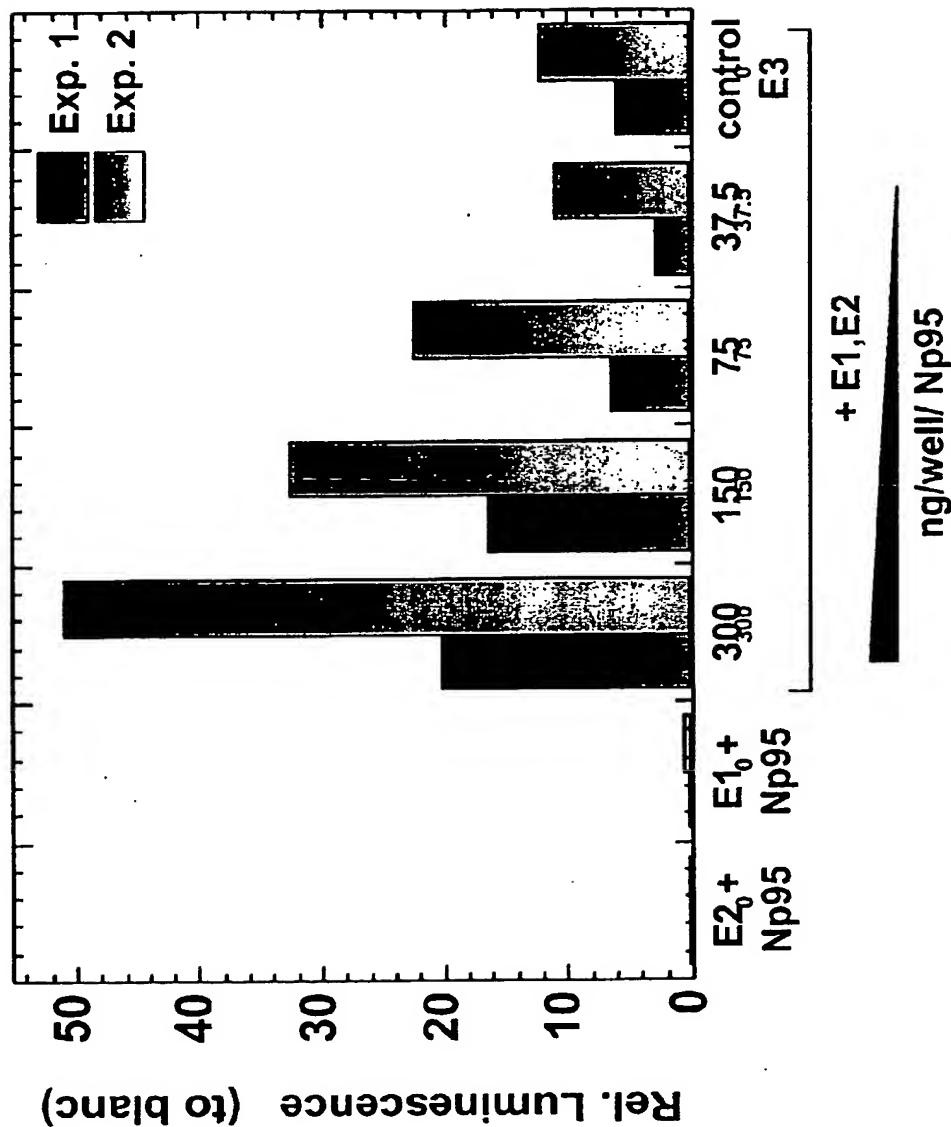
Add α-Flag HRP
conjugate to detect
the Flag-Ubiquitin

Read plate in luminometer

RIGEL

FIG. 62

Np95 Plate-based Auto-ubiquitylation Assay



Reactions contained 100 ng FI-Ub, 5 ng of E1 and, 20 ng of E2 per well. The Np95 controls contained 150 ng Np95. The E3 control contained 75 ng E3. The two data sets are results of duplicate assays.

FIG. 63

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